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ALIGNMENTS

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R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wondowsome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719

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                            A;Status: preliminary
A;Molecule type: DNA
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R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                           C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria
A;Reference number: A72200; MUID:99287316
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ine zipper.		3
<pre>phaseolin; PHA-L; bean; nuclear protein; promoter; ORF; bZIP;</pre>		KW
Pv-Seed factor-1; ROM1; Vicilin-box binding protein-1; ROM2; 7S-globulin;		3
<pre>ion factor; seed storage protein; lectin; oil-body protein;</pre>		~
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Amino acid sequence of bZIP2 ORF1 protein.		₽
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	C AAB48241;	AC.
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AAB48241 standard; Protein; 552 AA.	D AAB48241 sta	IJ
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                                                                                                                                                                                              Bodmer J,
Irmler M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated transcription factor gene which is expressed in a recombinant maturing dicot seed and which encodes a transcription factor protein which targets a promoter of a gene encoding seed storage proteins, lectins or oil-body proteins. The transcription factors isolated are Pv-Seed factor-1 (ROM1) and vicilin-box binding protein-1 (ROM2). These factors bind to 7s-globulin (b-phaseolin) or lectin (PHA-L) promoters. The transcription factor gene is useful for enhancing or reducing expression of seed storage protein, lectin or oil-protein genes in dicot seed crops. The present sequence represents the amino acid sequence of bZIP2 (basic leucine zipper) ORF1 protein.
This invention describes novel human and mouse anti-apoptotic gene products which contain at least one death effector domain. The products of the invention are used in the treatment of HIV infections and to the treatment of the human Herpes virus
                                                                                                                                                                                                                                                                                                                                                                                                                                      Death effector HIV infection;
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                                                                             Claim 16; Fig 16; 45pp; German
                                                                                                        New DNA encoding for anti-apoptotic infections and autoimmune diseases
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                                                                                                                                     mammary gland cells. The invention is useful for stimulating bovine mammary gland cell growth and function, inhibiting the growth of various mammary gland cancer cells, inhibiting
                                                                                                                                                                                                               New polypeptides and polynucleotides encoding the polypeptides, which are expressed in bowthe mammary gland tissue, useful for stimulating mammary gland growth or function, or inducing differentiation of milk producing cells
                                                                                             Sequence
                                                                                                                                                                     The present invention relates to proteins derived from bovine
                                                                                                                                                                                           Claim 11; Page 62;
                                                                                                                                                                                                                                                                                         Havukkala IJ,
                                                                                                                                                                                                                                                                                                                                             23-AUG-1999;
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                                                                                                                  growth of blood vessels in a mammal.
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09x2g3 thermotoga
006111 clostridium
09vfe9 drosophila
095309 sus scrofa
09vzu3 drosophila
09vzu3 drosophila
09vgu3 dictyosteli
09yfq8 aeropyrum p
09lrt3 arabidopsis
049807 mycobacteri
004919 saccharomyc
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Q9SLE9	090078	066264	Q59316	P87161	Q9F8X3	Q9KKT5	004473	Q9EYG4	P91783	Q903D1	067472	Q98240	P96312	Q9SIF1	Q9YCK9	Q9LR59	018860	018859	018857	Q15149	Q9QXS1	Q9M9T8	083125	Q9SZV1	097272
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ALIGNMENTS

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PRELIMINARY;	RTCVLGYLHIVPEFIESQLLGLLSP : : : :: RKCILDNLHWTFSQYEILGLLGP	36.9%; Similarity 44.0%; ll; Conservative	Hypothetical protein; Chloropiast. SEQUENCE 239 AA; 26836 MW; 58A	SMART; SM00382; AAA; 1.	Pfam; PF00005; ABC_tran; 1.	IPR003439;	IPR001687;	AF233069; AAF81686.1;	Submitted (FEB-2000) to the	(2393;	OM N.A.	100001	130081	Rhodophyta;	•	Galdieria sulphuraria.	按:	(TIEMBLIEL 15,	(TrEMBLrel.	· Management ,	PRELIMINARY:	
PRT;	SP 25 GP 36	Score 52; Pred. No. 5; Mismat	plast. 7; 58A28						EMBL/Gen			•		Lophyceae			Ī	Last seq		FAL,	DRT.	
688 AA.		DB 8; Length 239; 7.1; ches 7; Indels 2;	st. 58A2868B544A85FD CRC64;		NEW THE PROPERTY AND ADDRESS OF THE PROPERTY ADDRESS O			the state of the s	EMBL/GenBank/DDBJ databases					Bangiophyceae; Porphyridiales; Porphyridiaceae;			ammorarton abaara)	sequence update).	i u	AUG PER.	239 AA	
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-Q-/cgn2_1/USPTO_spool/US09251133/runat_06082001_175546_16481/app_query.fasta_1.84
-Q-/cgn2_1/USPTO_spool/US09251133/runat_06082001_175546_16481/app_query.fasta_1.84
-DB=EST -QFMT-fastap -SUFFIX-rst -GAPOP-12.000 -GAPEXT-4.000
-MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000 -GAPOP-4.000
-QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500 -DELOP-6.000
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -START-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-200000000 -USER-US09251133_@CGN1_1_2540 -NCPU-6
-ICPU-3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
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        en | Documentation ... 1808_T7A RPC 324 | AQ782752 HS_3301_A1_B08_T7A RPC 324 | AZ238007 RPCI-32-72819.TV RPCI-814 | BF341640 602016073F1 NCI_CGAP_B 699 | AZ366689 1M0116102F Mouse 10kb 499 | AW859667 RC4-CT0360-141299-011-487 | AQ880197 HS_5307_BL_G03_T7 RPCI 18004824 RC5-CN0132-211100-023-344 | BG004824 RC5-CN0132-211100-471-345 | BF745695 CM2_BT0857-021100-471-363 | BF745695 CM2_BT0857-021100-471-363 | BF710445 PM1-HT0628-130700-006-527 | AA291407 zt44e06.r1 Soares ovary 441 | B3695 yu38h07.r1 Soares ovary 441 | B3695 yu38h07.r1 Soares ovary 441 | B3695 yu38h07.r1 Soares ovary 441 | B4665 yu38h07
AA402524 zu48b06.rl Soares ova-
AA457266 au9301.xl Schneider;
BE910433 60150729fl NIH_MGC_7(
AL337675 Tetraodon nigrovirid;
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gb_est51:AW761339
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Similarity:
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
plate: 877 row: C column: 15
Seq primer: T7
Class: BAC ends
High quality sequence stop: 514.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Meller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
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genomic clone Plate=877 Col=15 Row=C, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          scanning the human genome
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AQ782752.1 GI:5685712
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                                                                                                                                                                 /note="Yector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen do and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

104 g 175 t 4 others
                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=877 Col=15 Row=C"
/clone_lib="RPCI-11 Human Male E
/sex="male"
  Percent
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AW761339 s166c01.y1 Gm-c1027
AA680210 ac82e01.s1 Stratage
AQ769011 HS_3191_A2_C11_MR C
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LOCUS AZ238007
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Percent Similarity:
                                                                                            Align seg 1/1 to: AZ238007
                                                                                                                                  US-09-251-133-6 x AZ238007
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 72 row: B column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Dr.,
Tel: 301 838 0200
Fax: 301 838 0208
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Other_GSSs: RPCI-23-72B19.TJ
Contact: Shaying Zhao
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RPCI-23-72B19.TV RPCI-23
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Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pleter de Jong [pieter@dejong.med.buffalo.edu]. Clones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ238007.1 GI:8546053
GSS.
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AZ238007
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                                                                                                                                                                                                                                                                                                                                                  /note-*Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "a 57 c 56 g 114 t
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/clone="RPCI-23-72B19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-23"
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LOCUS AZ366689
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Quality:
LOCUS AZ366689 699 bp DNA GSS 02-OCT-2000 DEFINITION 1M0116102F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Tlasue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9417 row: a column: 19
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High quality sequence stop: 707.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
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/clone=1ib="NMAGE:4151706"
/clone=1ib="NMAGE:4151706"
/tlssue_type="glioblastoma with EGFR amplification"
/tlssue_type="glioblasto
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                                                                         Align seg 1/1 to: AZ366689
                                                                                                                        US-09-251-133-6 x AZ366689
                                                                                                                                                                                            Percent Similarity:
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    1 ArgThrCysValLeuGlyTyrLeuHisIle...
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Ratio:
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University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly, N., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone UUGC1M0116I02 F, DNA sequence.
AZ366689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
1 (bases 1 to 699)
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ366689.1 GI:10480389
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                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
III :: : III : : : III III : : :
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                                                                                                                                                                                          58.50
2.925
57.143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="UUGC1M0116I02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male"
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alignment_block:
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Katsukuma, A., Bala, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW859667 499 bp mRNA EST 19-MAY-2000 RC4-CT0360-141299-011-d04 CT0360 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC4-CT0360-141 299-011-d04&t3=1999_12-14&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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                                                                                                                               Quality:
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Fax: +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                               Ratio:
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                                                                                                                                                                                                                                                 /note-"Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                       58.00
3.053
67.857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieteredejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 8805 row: N column: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ880197 487 bp DNA GSS 09-NOV-1999
HS_5037_B1_G03_T7 RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=8805 Col=5 Row=N, DNA sequence.
                                                                                                                                      Quality:
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Class: BAC ends
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1 (bases 1 to 487)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Mahairas,G.G., Wallace,J.C., Young,J., Zhao,S., Adams,M.D. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 487 
Location/Qualifiers
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                                                                                                                                                                                                                            /note-"Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI
Male blood DNA was isolated from one randomly chosen
and partially digested with a combination of EcoRI an
EcoRI Methylase. Size selected DNA was cloned into th
pBACe3.6 vector at EcoRI sites"

1 others
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=8805 Col=5 Row:N"
                                                                                               57.50
2.875
83.333
                                                                                                                                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI-11 Human Male BAC Library"
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1 (bases 1 to 344)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.bb/scripts/gethtml2.pl?tl=RC5&t2=RC5-GN0132-211100-023-A04&t3=2000-11-21&t4=1)
Seq primer: puc 18 forward seq primer: puc 18 forward to the project of the project 
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Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                    /note-"Organ: placenta_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/db_xrefe"taxon:9606"
/clone_libe"GN0132"
/dev_stage="Adult"
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|CTGCATATAACTCCGGACCATATACAGCTCCAACTACTGGGCTTAATTTC 106
                                                                                                                                               Quality:
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-BT0857-
021100-471-e07&t3=2000-11-02&t4=1)
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Fax: +55-11-2707001
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
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  to reverse of: BF745695
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/db_xref="taxon:9606"
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seq_name: gb_est92:BF763364
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                                                                                                                          Quality:
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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x BF763364/rev
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                                                                                                                                                                                                                                                                                                                     /note="Organ: colon_est; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                            tissue mRNA and cDNA amplification were performed under low stringency conditions." 123 c 122 g 100 t
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/clone_lib="CS0038"
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1 (bases 1 to 491)

Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Seq primer: puc 18 forward
High quality sequence stop: 359.
Location/Qualifiers
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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  to reverse of: BE710443
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/db_xref="taxon:9606"
/clone_lib="HT0628"
/dev_stage="Adult"
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                                                                                                   Quality:
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Possible reversed clone: similarity on wrong strand Insert Length: 791 Std Error: 0.00 Seq primer: -28ml3 rev2 Er from Amersham High quality sequence stop: 446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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AA291407
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                                                                                  Ratio:
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/db_xref="taxon:9606"
/clone-"IMAGE:725218"
/clone_lib-"Soares ovary tumor NbHOT"
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REFERENCE
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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1 (bases 1 to 547)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Glsh,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry,Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags of 200,000 human expressed sequence tags of 200,000 human expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <code>yu38h07.r1</code> Soares ovary tumor NbHOT Homo sapiens cDNA clone <code>IMAGE:236125 5'</code>, <code>mRNA</code> sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stops: 361
Source: IMAGE Consorthum, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 953 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
Insert Size: 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
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Location/Qualifiers
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314 286 1810
                                                                                                                                                         (Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo. "
137 c 134 g 143 t 10 others
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/clone="IMAGE:236125"
                                                                                                                                                                                                                                                                                                                     /tissue_type="ovarian tumor" resistant)"/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="GDB:3863044"
                                                                                                                                                                                                                                                                                                                                                                        /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares ovary tumor NbHOT"
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Quality:

57.00

Length:

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alignment_scores:

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US-09-251-133-6 x H53695
BASE COUNT
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA402524 645 bp mRNA EST 09-NOV-1997 zu48b06.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741203 5' similar to TR:G608464 G608464 RIBONUCLEOPROTEIN. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@mage.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Insert Length: 810 Std Error: 0.00 Stg primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Mart,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 508
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
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: 88.235
                                                                                                (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                               the Not I and Eco RI sites of a modified pT7T3 vector
                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:5941239"
/db_xref="taxon:9606"
/clone="IMAGE:741203"
                                                                                                                                                                                                                          /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                      /sex="Female"
                                                                                                                                                                                                                                                                                        /clone_lib="Soares ovary tumor NbHOT"
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KEYWORDS
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VERSION
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US-09-251-133-6 x AA402524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.lln1.gov) for further information. Seq primer: -40Up from Gibco High quality sequence stop: 473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 660)
Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptce,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
Washd-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW157266 660 bp mRNA EST 04-NOV-1999 au93g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783856 3' similar to TR:043251 043251 HYPOTHETICAL 39.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
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AW157266
AW157266.1 GI:6228667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
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                145
/note="Organ: brain; Vector: pBluescript SK (Stratagene); Site_1: SstI; Site_2: XhoI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor
                                                                                                                                                                                                                                                                                                             /tissue_type="frontal lobe"
/dev_stage="5 months post-conception"
/lab_host="DHIOB"
                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2783856"
                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Schneider fetal brain 00004"
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3.800
88.235
                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
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Gaps: 0
Identity: 64.706
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                                                                       Library
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VERSION
KEYWORDS
alignment_block:
US-09-251-133-6 x BE910433/rev
                                                                                                                alignment_scores:
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LOCUS BE910433
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US-09-251-133-6 x AW157266
                                                                                                                                                                                         BASE COUNT
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                                                         Percent Similarity:
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 818)

1 (bases 1 to 818)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9712 row: j column: 07
High quality sequence stop: 572.
Location/Qualifiers
                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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601503729F1 NIH_MGC_70
mRNA secure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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BE910433
BE910433.1 GI:10407019
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
187 c 220 g 178 t
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3.800
88.235
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Database length: 94655562
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-Q-/cgn2_1/USPTO_spool/US09251133/runat_06082001_175547_16513/app_query.fasta_1.84
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-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GGAPEXT=0.050 -GAPEXT=7.005 -XGAPOP=10.000 -XGAPEXT=0.500
-GGAPEXT=0.000 -GAPEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -GAPEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=200000000
-USER=US09251133_@CGN1_1_50 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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US-09-251-133-6 x US-09-176-657-5/rev
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; OTHER INFORMATION: 1250374
US-09-176-657-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-348-353-16
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LENGTH: 1506
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Apr---
Sequence 16, Apr---
Sequence 16, Apr---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PERL Program
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tuomanen, Elaine APPLICANT: Masure, Robert TITLE OF INVENTION: Antibod TITLE OF INVENTION: Ligand NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  808 C
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                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 LeuHisIleValProGluPheIleGluSerGlnLeuLeuGlyLeuLeuSe 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
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3.800
88.235
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Percent Identity:
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from: 1 to: 1506

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/cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-403-866-11 + /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-557-309B-21 - /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-98-34-306-21 - /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-993-674A-21 - /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-07-851-976B-7 - /cgn2_6/ptodata/1/ina/5A_COM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lu, Aina
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
FILE REFERENCE: PF-0611 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/176,657
CURRENT FILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 9
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121.51
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alignment_block:
US-09-251-133-6 x US-08-348-353-16/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-348-353-16
                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Tuomanen, Elaine
APPLICANT: Massure, Robert
TITLE OF INVENTION: Antibody F
TITLE OF INVENTION: Ligand for
NUMBER OF SEQUENCES: 38
CORRESPONDENCE, ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: US-08-348-353-16
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                                                                                                                                                                                                                                                                                                                                Sequence 16, Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VOLUME: 9
ISSUE: 9
PAGES: 2895-2905
^*TE: September-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
ZIP: 07bui
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1925 ACCTGCATCTTGCCCGCGTTGCGCGCGCCCCGGAAGTCGTCAGCGTGGC 1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1875 GCTCTTGGCCATGACCTCGGCCCCGGTCTCGTTG 1842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 1..3744
PUBLICATION INFORMATION:
AUTHORS: Delisse-Gathoye, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348 257
FILING DATE: 30-NOV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Jackson, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 nLeuLeuGlyLeuLeuSer...ProValSerLeu 28
                                                                                                                   STREET: 411 Hack
CITY: Hackensack
STATE: New Jerse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                               COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE: Cloning, Partial Sequence, Expressions, and
TITLE: Antigenic Analysis of the Filamentous
TITLE: Hemagglutinin Gene of Bordatella Pertussis
                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL:
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                                                                                                                                                                                                                                                                                                                                    6, Application US/08465965
5968512
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                                                                                                               New Jersey
                                                                                                                                                        411 Hackensack Avenue
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                                                                                                                                                                            Klauber & Jackson
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71.429
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seq_documentation_block:
; Sequence 16, Application US/08465966
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US-09-251-133-6 x US-08-465-965-16/rev
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Quality:
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; DATE: September-1990
US-08-465-965-16
                                                               seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-465-966-16
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TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
                                                                                                          1875 GCTCTTGGCCATGACCTCGGCCCCGGTCTCGTTG 1842
                                                                                                                                                                                            1925 ACCIGCATCITGCCCCGCGTTGCGCCCCGGAAGTCGTCAGCGTGGC 1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..3744

PUBLICATION INFORMATION:
AUTHORS: Delisse-Gathoye, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 04-MAY-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/695,613
FILING DATE: 03-MAY-1991
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 08/348,353
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 3744 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/247,572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                   18 nLeuLeuGlyLeuLeuSer...ProValSerLeu
                                                                                                                                                                                                                                       2 ThrCysValLeuGlyTyrLeuHisIleValProGluPheIleGluSerGl 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE: Cloning, Partial Sequence, Expressions, and TITLE: Antigenic Analysis of the Filamentous TITLE: Hemagglutinin Gene of Bordatella Pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson, David REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US92/03725 FILING DATE: 04-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Infection and Immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-1995
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2.625
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                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 46.429
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Patent No. 6015560

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alignment_scores:
Quality:
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 Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 07601
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: FLOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,966
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tuomanen, Elair
APPLICANT: Masure, Robert
TITLE OF INVENTION: Antibo
TITLE OF INVENTION: Ligan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jackson, David REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-097CIP1DIV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 23-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hackensack
STATE: New Jerse
                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/
FILING DATE: 04-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/3 FILING DATE: 30-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/695,613
                                                                                                                                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                JOURNAL:
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                                                                                                                         September-1990
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                                                                                                                                                                                                           Cloning, Partial Sequence, Expressions, and Antigenic Analysis of the Filamentous Hemagalutinin Gene of Bordatella Pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 Hackensack Avenue
                                                                                                                                             2895-2905
                                                                                                                                                                                                                                                                                                                                                                                                          3744 base pairs
                                                                                                                                                                                                                                                                    Delisse-Gathoye,
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                                                                                                                                                                                                Infection
                                                                                                                                                                                                                                                                                                                                                        linear
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52.50
2.625
71.429
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Percent Identity:
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                                    Length:
 46.429
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alignment_block:
US-09-251-133-6 x US-08-666-798-1/rev
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US-09-251-133-6 x US-08-465-966-16/rev
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                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                            US-08-666-798-1
                                                                                                              Align seg 1/1
                                                                                                                                                                                                         Percent Similarity:
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Patent No. 5648238
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1875 GCTCTTGGCCATGACCTCGGCCCCGGTCTCGTTG 1842
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,
FILING DATE: FILED HEREWITH
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: c
IMMEDIATE SOURCE:
LIBRARY: CONSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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MEDIUM TYPE: Diskett
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                                     292 AGGAGTTGCCTGCTGGGCCTTGGCCACTTCATTCCTCATCAGTCACACCT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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17 rGlnLeuLeuGly 21
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CITY: Palo Alto
STATE: CA
                                                                       1 ArgThrCysValLeuGlyTyrLeuHisIleValProGluPheIleGluSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Luther, Barbara REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic
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                                                                                                                                                                                                                                               Quality:
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                                                                                                            to reverse of: US-08-666-798-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       640 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                   linear
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3.188
76.190
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Percent Identity: 47.619
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                                                                                                              to: 640
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242 GCAGCTCCTCGGA 230

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seq_documentation_block:
                                                   seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-09-096-071-1
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US-09-251-133-6 x US-08-892-692-1/rev
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Quality:
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                                                                                                                                                                                                                                            Align seg 1/1 to reverse of: US-08-892-692-1 from: 1 to: 640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                          242
                                                                                                                                                                     292 AGGAGTTGCCTGCTGGCCTTGGCCACTTCATTCCTCATCAGTCACACCT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS LENGTH: 640 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                            17 rGlnLeuLeuGly 21
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CITY: Palo Alto
STATE: CA
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
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ZIP: 94304
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                                                                                          GCAGCTCCTCGGA 230
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3174 Porter Drive
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: 47.619
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MOLECULE TYPE: cl
; IMMEDIATE SOURCE:
; LIBRARY: CONSEI
US-09-096-071-1
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Quality:
                                                                                                                              seq_documentation_block:
                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/1na/6B_COMB.seq:US-08-796-899-26
                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: US-09-096-071-1
                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                          Sequence 26, Application US/08796899 Patent No. 6160202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09096071 Patent No. 5879893
GENERAL INFORMATION:
APPLICANT: BUSTOS, Mauricio M
APPLICANT: CHERN, Maw-Shenq
TITLE OF INVENTION: MODIFICATION OF SEED CROPS WITH
TITLE OF INVENTION: TRANSCRIPTION FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: AU-YOU
APPLICANT: HAWKIN
APPLICANT: HILLMA
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                    242 GCAGCTCCTCGGA
                                                                                                                                                                                                                                                                           292 AGGAGTTGCCTGGGCCTTGGCCACTTCATTCCTCATCAGTCACACCT 243
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APPLICATION NUMBER:
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APPLICANT: HAWKINS, PHILLIP R.
APPLICANT: HILLMAN, JENNIFER L.
TITLE OF INVENTION: HUMAN PROTEIN KINASE C INHIBITOR HOMOLOG
                                                                                                                                                                                                                                        17 rGlnLeuLeuGly 21
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                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/096,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            640 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415-845-4166
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linear
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3.188
76.190
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                                                                                                                                                                                                                                                                                                                                                 from: 1
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: 0
: 47.619
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NUMBER OF SEQUENCES:

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alignment_block:
US-09-251-133-6 x US-08-796-899-26
                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-352-159-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: DNA (genomic) US-08-796-899-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECUTE (703) 836-2021
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
TENGTH: 1657 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-796-899-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                  Sequence 1, Application US/09352159A Patent No. 6211434 GENERAL INFORMATION:
                                   APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
EARLIER FILING DATE:
                        EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/319,544
FILING DATE: 07-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 CTATTGGGCCACATTCACACGGTCAAGGAGTTCCATCCCCACCTGCTGCT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                        20 uGlyLeuLeu 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 06-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                           GGGACTCCTT 420
APPLICATION NUMBER: 60/135,391 FILING DATE: 1999-05-21
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: United States
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3.643
70.000
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; LOCATION: (346)...(346); OTHER INFORMATION: n = A,T,C or US-09-352-159-1
                                                                           alignment_block:
US-09-251-133-6 x US-09-352-168-1
                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; LCCATION: (346)...(346)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-168-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-251-133-6 x US-09-352-159-1
                                                                                                                                                                                                       alignment_scores:
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Percent Similarity:
                                      Align seg 1/1 to: US-09-352-168-1
                                                                                                                                          Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1
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Sequence 1, Apr. 5211435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 0875
CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 46 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gilliam, Jacob T.

APPLICANT: Maddox, Joyce R.

TITLE OF INVENTION: Amino Polyol Amine Oxidase

TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Crasta, Oswald R. APPLICANT: Duvick, Jonathan P. APPLICANT: Folkerts, Otto
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TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                      LENGTH: 372
TYPE: DNA
ORGANISM: Exophiala spinifera.
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 TGGACTGTTGGGACCACTT 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 CTCGTAGGCTGCGCGGAGTTGGTCCCAGACAGACTTTTGTCGTACCTGCT
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4 ValLeuGlyTyrLeuHisIleValProGluPheIleGluSerGlnLeuLe 20
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                                                                                                                                                                                   Quality:
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Gaps: 0
Percent Identity: 43.478
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                                         from: 1
                                      to: 372
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alignment_block:
US-09-251-133-6 x US-09-352-159-5/rev
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; LOCATION: (1)...(1386)
US-09-352-159-5
                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/1na/6B_COMB.seq:US-09-352-168-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
GENERAL INFORMATION:
APPLICANT: Crasta, Oswald R.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Folketts, Otto
APPLICANT: Folketts, Otto
APPLICANT: Haddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 0875
CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: US-09-352-159-5
                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09352168A Patent No. 6211435
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Patent No. 6211434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 5 LENGTH: 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/92,936
EARLIER FILING DATE: 1998-07-25
EARLIER FILING DATE: 1998-07-25
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
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APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1125 CTCGTAGGCTGCGCGGAGTTGGTCCCAGACAGACTTTTGTCGTACCTGCT 1076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1075 TGGACTGTTGGGACCACTT 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ValLeuGlyTyrLeuHisIleValProGluPheIleGluSerGlnLeuLe 20 ::::::||| ::: ||| |||||
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2.722
78.261
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                            Align seg 1/1
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NAME/KEY: CDS
LOCATION: (1)...(1389)
NAME/KEY: misc_feature
LOCATION: (1)...(3)
COTHER INFORMATION: Extra lysine in K:trapao
US-09-352-159-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Pol
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
                                       alignment_block:
US-09-251-133-6 x US-09-352-159-10/rev
                                                                                                                                               alignment_scores:
Quality:
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US-09-251-133-6 x US-09-352-168-5/rev
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Quality:
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; LOCATION: (1)...(1386)
US-09-352-168-5
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                                                                                                     Ratio:
Percent Similarity:
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Percent Similarity:
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SOFTWARE: FRATSEQ for Windows Version 3.0

SEQ ID NO 5

LENGTH: 1389

TYPE: DNA

ORGANISM: Exophiala spinifera
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 10
LENGTH: 1392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/09352159A Patent No. 6211434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1125 CTCGTAGGCTGCGCGGAGTTGGTCCCAGACAGACTTTTGTCGTACCTGCT 1076
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Exophiala spinifera
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                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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to reverse of: US-09-352-159-10
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Percent Identity:
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Percent Identity: 43.478
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from: 1
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alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-352-159-7
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Percent Similarity:
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                                                                                                                                                                                                                             Sequence 7, Application US/09352159A Patent No. 6211434
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                                            APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related
FILE REFERENCE: 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Folkers, Otto
APPLICANT: Holkers, Otto
APPLICANT: Haddox, Jocob T.
APPLICANT: Maddox, Jocob T.
APPLICANT: Maddox, Jocob T.
APPLICANT: MINOR Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 0875
CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT FILLING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILLING DATE: 1998-07-25
NUMBER OF COLUMN NUMBER: 1998-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Crasta, Oswald R. APPLICANT: Duvick, Jonathan P.
CURRENT APPLICATION NUMBER: US/09/352,159A CURRENT FILING DATE: 1999-07-12
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NAME/KEY: CDS
LOCATION: (1)...(1389)
NAME/KEY: misc_feature
LOCATION: (1)...(3)
OTHER INFORMATION: Extra lysine in K:trapao
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1078 TGGACTGTTGGGACCACTT 1060
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ORGANISM: Exophiala spinifera
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                                                                       Polypeptides and Methods of Use
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alignment_block:
US-09-251-133-6 x US-09-352-159-7/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 14
TYPE: DNA
20 uGlyLeuLeuSerProVal 26
||||||||||:::|||:::
1128 TGGACTGTTGGGACCACTT 1110
                                                                                  1178 CTCGTAGGCTGCGCGGAGTTGGTCCCAGACAGACTTTTGTCGTACCTGCT 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Exophiala spinifera FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: intron
LOCATION: (647)..
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LOCATION: (1)...(646)
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Gaps: 0
Percent Identity: 43.478
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jb_in1:AC009219
gb_htg21:AL357506
gb_in2:AE003688
gb_htg3:AC011538
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gb_pr3:AC009237
gb_pr3:AC009948
gb_htg14:AC068960
gb_htg14:AC068960
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gb_htg12:AC039238
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gb_htg2:AC009984
gb_htg4:AC013977
gb_in1:AC008140
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gb_htg4:AC013565
gb_htg2:AC009728
gb_htg1:AC006903
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gb_p11:AF129022
gb_pr5:AL135917
gb_in1:AC025716
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gb_htg21:AL356986
gb_htg13:AC055784
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gb_p11:AF129024
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gb_pr6:AL139343
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Query length:
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gb_pr8:HS41P2
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Database length: -856060004
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-Q-/ggn2_1/USPTO_spool/US09251133/runat_06082001_175546_16494/app_query.fasta_1.84
-Q-/ggn2_1/USPTO_spool/US09251133/runat_06082001_175546_16494/app_query.fasta_1.84
-DB-GenEmb1 -QFMT-fastap -SUFFIX--ge -GAPOP-12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCLT_0.000 -LOOPEXT=0.000 -GAPOP-4.500
-QGAPEXT=0.050 -XGAPOP-10.000 -XGAPEXT=0.500 -FGAPOP-6.000
-FGAPEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500 -DELOP-6.000
-DELEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500 -THR_MIN=0
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN=0
-MAXLEN=200000000 -USER-US09251133_@CGN1_1_4284 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
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I AL356986 Homo sapiens chromo
I AC055784 Homo sapiens chromo
I AC007115 Homo sapiens chromo
I AC013565 Homo sapiens chromo
I AC013565 Homo sapiens chromo
I AC009728 Homo sapiens chromo
I AC00903 Caenorhabditis eleg
AC009984 Drosophila melanogal AC013977 Drosophila melanogal AC013977 Drosophila melanogal AC008140 Drosophila melanogal AC009219 Drosophila melanogal AC009219 Drosophila melanogal AC01538 Homo sapiens chromosis AC021990 Homo sapiens chromosis AC021990 Homo sapiens chromosis AC021990 Homo sapiens chromosis AC021990 Homo sapiens chromosis AC021484 Homo sapiens chromosis AC021412 Homo sapiens chromosis AC021412 Homo sapiens chromosis AC021413 Homo sapiens chromosis AC019339 Homo sapiens chromosis AC019339 Homo sapiens chromosis AC019337 Homo sapiens clone AC019337 Homo sapiens BAC clipacological AC019348 Homo sapiens BAC clipacological AC0193484 Homo sapiens BAC clipacological AC01934848
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1 AL355389 Homo sapiens chrom
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AC02571
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917 Human DNA seguenc
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16 Caenorhabditis elec
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gb_pl1:AF129039
gb_pr9:HSP38A20
gb_ro1:MUSAREC3B
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AUTHORS
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seq_documentation_block: LOCUS HS41P2A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The true left end of clone 41P2 is at 1 in this sequence. The true right end of clone 106120 is at 45063. This sequence from clone 41P2 has been finished in more than one contig. This sequence (41P2h) is separated from the following one (41P2B Z81314) by a gap of 100bp sized by restriction analysis. 41P2 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pleter de Jong.

For further details see http://bacpac.med.buffalo.edu/ VECTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pCYPAC2 This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              such as compressions and repeats, but not necessarily within kno annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone requests: clonerequest@sanger.ac.uk
IMPORTANT: This sequence is not the entire insert of clone 41P2.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 47329)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-OCT-1996) E-mail enquires: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z81357.1 GI:1648867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            feature key.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence has been finished according to sequence map criteria ollows. An attempt is made to resolve all sequencing problems
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                                                                       /note="L1MC3 repeat: 3890. .4188
                                                                                                                                                                                       2044 .2346
/note="AluSq repeat: matches 303...l of consensus"
2427 .2656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RPCI1" 63. .359
/note="AluSx repeat: matches 299.
4739. .4898
/note="L1 repeat: matches 1721. ...
                                                                                                                                                                                                                                                                                                                                                                                           /note="FLAM_A repeat: matches 1. .133 of consensus"
719. .887
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluSq repeat: matches 296.
387. .519
                                                                                                                                                                                                                                                                      /note="AluSq repeat:
                                                                                                                                                                                                                                                                                                                      1069. .1112
/note="22 co
                                                                                                                                                                                                                                                                                                                                                                    /note="MIR repeat: matches 40. .214 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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57.00
                                                                                                                                                                                                                                                                                                                      copies of 2 mer 82 % conserved"
  repeat: matches 1721. .1882 of consensus*
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                                                                                                                                                                                                                                                                        matches 302.
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667 | AF129039 Nemuaron vieillardi
1876 | ALO09266 H. sapiens cDNA si:
1955 | D50417 Mouse mRNA for AREC3
                                                                                                   2486.
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                                                                                                                                                                                                                                                                        /note="Alusx repeat: matches 298...1 of consensus"
30644...30944
/note="Alusx repeat: matches 1...302 of consensus"
/note="Alusx repeat: matches 1...302 of consensus"
32056...32609
32056...32609
/note="match: 3' EST H12785 clone 148765; Paired with 12846 matching this clone"
complement(<232599...33072)
/note="match: 5' EST H12846 clone 148765; Paired with 12845 matching this clone"
                                                                                                                                                                                                                           32761. .32834
/note="2 copies of 37
35883. .36271
                                                                                                            /note-"7 copies of 4 mer 93 % conserved" complement(<38272. .38643) /note-"match: 5' EST H71902 clone 214840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluSp repeat: matches 1. .51 of c 6854. .7046  
/note="LIME3A repeat: matches 707. .908
                                    /note="AluY
39366. .396
                                                                                     /note-"match: 5' EST H71902 clone 214840;
H71901 matching this clone"
                                                                                                                                                                     37474.
                                                                                                                                                                                  /note="match: 5' EST H71901 clone 214840; Paired H71902 matching this clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Aluy repeat: matches 300. .2 of consensus" 29874. .30169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="14 copies of 2 mer 93 % conserved" 28846. .29145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19873
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join(<11736. .11849,15371. .15424,25100. .25192,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22890.
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225303 clone B7F03; match: 5' EST H53695 clone 236125"
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/note="AluSx repeat: matches 1.
$3904. .43939
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14549. .14793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MER5B repeat: matches 178. .1 of consensus"
12606. .12787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10829.
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join(8298. .8333,8364. .8404)
/note="Pro-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note-"MIR repeat: matches 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MLT1D repeat: matches 505. .6 of consensus"
22890. .22951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L1MA4A repeat: matches 1047. .887
20906. .21174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSx repeat: matches 302. .1 of consensus"
19873. .20027
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13061. .13100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluJb repeat: matches 2.
5610. .6770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note-"MER33 repeat: matches 41. .312 of consensus"
                               ALUY repeat: matches 1.
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                                                                         .39353
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                                                      .296 of consensus
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                 .302 of consensus"
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                      feature key.
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Align seg 1/1 to reverse of:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw.; SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Cione requestes: clonerequestesanger.ac.uk
On Dec 13, 1999 this sequence version replaced g1:4741471.
                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP1-41P2 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was generated from part of bacterial clone contigs human chromosome 22, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 108315)
                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/HGP/Chr22
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repeat_region 74297653 /note="3 copies 19 mer 84 conserved" /note="3 copies 75 mer 75 conserved" repeat_region 75937896 /note="4 copies 76 mer 83 conserved" repeat_region 78287959 /note="2 copies 66 mer 85 conserved" repeat_region 79948143	367 367 367 367 367 367 37 37 37 37 37 37 37 37 37 37 37 37 37	at: matche 76 mer 81 73 mer 84 74 mer 82 76 mer 64 75 mer 92	consensus" consensus" /note="MER81-internal consensus" region 4222. 4340 /note="MEE57-internal consensus" 4570. 4853 /note="14105 repeat: m region 4854. 4933 /note="20 copies 4 mer region 4875. 4930 /note="77 copies 8 mer region 4940. 5053 /note="MER95 repeat: m region 5930. 6082	repeat_region 1.160 //clone_lib="RPCI-1" //clone_li	http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2 IMPORTANT: This sequence is not the entire insert of clone RP1-41P2 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions. The true right end of clone RP1-41P2 is at 108315 in this sequence. The true left end of clone RP1-108120 is at 63252 in this sequence. I 108315 Location/Qualifiers source /organism="Homo sapiens" /chromosome="22" /chromosome="22" /chromosome="22" /chromosome="22"
repeat_region repeat_region repeat_region repeat_region	י לי לי לי לי	* * * * * * * *	repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region		
/note="2 copies 75 mer 83 conserved" 14040. 14267 /note="3 copies 76 mer 82 conserved" 14198. 14329 /note="2 copies 66 mer 84 conserved" 14368. 14517 /note="2 copies 75 mer 88 conserved"	ω. ω. α	.12753 .3 copies .12875 .2 copies .12976 .2 copies .13052 .13128 .2 copies .13207 .2 copies .13207	1.10988 1 copies 19 mer 76 1.11226 1 copies 77 mer 65 1.11513 1 copies 76 mer 81 1.11891 2 copies 78 mer 85 1.2113 1 copies 75 mer 72 2 copies 75 mer 72 1.2460 1.2591		/note="2 copies 75 mer 88 conserved" 8072. 8223 /note="2 copies 76 mer 87 conserved" 8375. 8596 /note="3 copies 74 mer 77 conserved" 8729. 8880 /note="2 copies 76 mer 86 conserved" 8810. 8969 /note="2 copies 80 mer 83 conserved" 8898. 9122 /note="3 copies 75 mer 77 conserved" 9068. 9195 /note="3 copies 64 mer 83 conserved" 9147 9374

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REFERENCE
AUTHORS
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VERSION
KEYWORDS
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Quality:
Ratio:
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                                                                                              Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 114021 bases at least Q40
Consensus quality: 117105 bases at least Q30
Consensus quality: 119164 bases at least Q20
Insert size: 131056; sum-of-contigs
Insert size: 139683; 7.0% error; agarose-fp
Quality coverage: 3.50x in Q20 bases; sum-of-contigs Quality
coverage: 3.13x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Aug 12, 2000 this sequence version replaced gi:9213547.
                                                                                                                                                                                                                                                                                                Center project name: dJ740B20
----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                   Center: Sanger Centre
Center code: SC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 122656)
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                                                                                                                                                                                                                                                                                                                                                            Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL355389.2 GI:9797294
NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                site:
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/notes 2 copies 76 mer 8

14832. .15001

/notes 2 copies 85 mer 8

15021. .15170

/notes 2 copies 75 mer 9

15094. .15397

/notes 4 copies 76 mer 8

15373. .15672

/notes 4 copies 75 mer 7

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17529 22644: contig of 5116 bp in length
22645 22744: gap of 100 bp
22745 24984: contig of 2240 bp in length
24985 25084: gap of 100 bp
25085 27553: contig of 2469 bp in length
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                                                                                                                                              25085. .27553
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  /note-"assembly_fragment:00516"
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42: gap of 100 bp
42: gap of 5607 bp in length
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8340: contig of 5896 bp in length
0: gap of 100 bp
13714: contig of 5274 bp in length
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77456: contig of 7860 bp in length
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contig of 2246 bp in length
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                                                                                                                                                                                                                                                               on Sep 11, 2000 this sequence version replaced gi:10039534. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                         The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                       This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (09-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequestssanger.ac.uk
                    numbers given in the feature table wi
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREME
on the WORMPEP database can be found
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Mammalia; Eutheria;
1 (bases 1 to 1448)
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http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
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88450. .96215
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82743. .88349
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/note="assembly_fragment:00538"
77557. .82642
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106793. .122656
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eria; Primates; Catarrhini; Hominidae; Homo.
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VECTOR: pCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is the entire insert of clone RP5-1078M7 The true left end of clone RP4-740B20 is at 74390 in this sequence. The right end of clone RP5-1155K23 is at 18613 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
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                                                                                                  /note="1
9619. .9
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                                                                                                                                                                                                                                                                    9069.
                   /note="match: GSS: Em:AQ366486"
complement(9807. .10272)
                                                                                                                                                                                                                                                                                                           /note="AluJb repeat: matches 3. 8936. .9057
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6413. .6719
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                                                         /note="12 copies 12 mer 77% conserved"
complement(9761. .10266)
                                                                                                                                                                                     9609.
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7377. .7591
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4734. .4852
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complement(148. .418)
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/note="MIR repeat: matches 178.
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/db_xref="taxon:9606"
/note="match: GSS: Em:AQ174667"
                                                                                                                                                              note="43 copies 4 mer tctc 73% conserved"
                                                                                                                                                                                                    note="96 copies 2 mer tc 70% conserved"
                                                                                                                                                                                                                                                 /note="5
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                                /note="24 copies 4 mer 25149. .25216
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15783 15870
/note="2 copies 44 mer 90% conserved"
16734 16800
                                                                                                                                                                        /note-"AluSx repeat: matches 1. complement(23992. .24251)
                                                                                                                                                                                                           /note="MER91A repeat: matches 6. 22118. .22422
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21153. .21217
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13773. .13855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="L1PB3 repeat: matches 5666. 11984. .12348
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L2 repeat: matches 2495.
19176. .19352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"match: GSS: 17259. .17394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AluSx repeat: matches 1. .290 of consensus"
14565. .14873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /notee MIR repeat: matches 68. .149 of consensus 14174. .14462
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/note="match: GSS: Em:AQ473771"
10485. .10791
                'note="34 copies 2 mer
                                                                   /note="match: GSS: 25148. .25243
                                                                                                       /note="match: GSS: 24276. .24713
                                                                                                                                        /note="match: GSS: 24276. .24717
                                                                                                                                                                                                                                                                /note="17 copies 2 mer ac 82% conserved"
                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 112.
21648. .21681
                                                                                                                                                                                                                                                                                                                                                                                                  note-"L2 repeat: matches 2304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15665. .15763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 57. .68 of consensus"
13468. .13772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: GSS: Em:AQ010332"
13456. .13467
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13204. .13605
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11909. .11919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="12 repeat: matches 2588. .2710 of consensus"
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11307. .11423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note-"MIR repeat: matches 107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="AluSg repeat: matches 1. .295 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   notes MIR repeat: matches 81.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-"MIR repeat: matches 31, .233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note-"AluJb repeat: matches 1. .308 of consensus"
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                                                                                                                      Em: AQ450746"
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                75% conserved"
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US-09-251-133-6 x AL139343
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                           JOURNAL
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                            IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc. . . eyen if efforts are made to eliminate these phage, etc. . . eyen if efforts are made to eliminate these
                                                                                                                                                                                                                                   - Web : www.genoscope.cns.fr)
On Jan 26, 2001 this sequence version replaced
------ Genome Center
                                                                                                                                                           Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                        Submitted (24-JAN-2001) Genoscope - Centre National de Seque
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 196023)
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HTG; HTGS_PHASE2; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome 14 clone R-173D9, PROGRESS ***, in ordered pieces.
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                                                                                                                                                                                                 Center code: GS
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               contaminating sequences. The following BAC sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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26771. .27
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/note="5 copies 17
25685. .25825
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/note="5 copies 16
25194. .25292
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3.200
83.333
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26351. .26472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note: "AluSq repeat: matches 1.
26115. .26189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note:"MIR repeat: matches 8. .179 of consensus" 25826. .26114
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to the SP6 end
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alignment_block:
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                     rGlnLeuGlyLeuLeuSerProValSer 27
                                              AGAGGCTGTGTTTGGTGGTACATGCATGTAGTCCCAGCTACCTGGGATGC
                                                                  ArgThrCysValLeuGlyTyrLeuHisIleValProGluPheIleGluSe 17
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                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Overall quality chart :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: Phrap; version 2.0 Quality coverage: 7.09x in Q20 bases; sum-of-contigs
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Downstream BAC
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                                                                                                                                                                                                                                                                                  RHdb:RH74629
                                                                                                                                                                                                                                                                                                                                          dbSTS:STS5516
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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US-09-251-133-6 x AF129033
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Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; Laurales; Monimiaceae; I
1 (bases 1 to 656)
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Laureliopsis philippiana
                                                Circumscription and phylogeny of molecular and morphological data Am. J. Bot. (1999) In press
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Direct Submission
Submitted (14-FEB-1999) Biology, Univ. of Missouri-St. Louis, 8001
Natrual Bridge Rd., St. Louis, MO 63121, USA
Location/Qualifiers
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Chloropiast Laureliopsis philippiana
Chloropiast Laureliopsis philippiana
Eukaryota, Viridiplantae, Embryophyta; Tracheophyta;
Magnoliophyta; Laurales; Monimiaceae; Laureliopsis.
Renner, S.S.
Direct Submission
                                                                                                Renner, S.S.
                                                                                                                                                                                   Laurelia novae-zelandiae.
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84 c 109
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/db_xref="taxon:74877"
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Chloroplast Doryphora sassafras
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnollophyta; Laurales; Monimiaceae; Doryphora.
1 (bases 1 to 657)
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Submitted (14-FEB-1999) Biology, Univ. of Missouri-St.
Natrual Bridge Rd., St. Louis, MO 63121, USA
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Doryphora sassafras chloroplast trnT-trnL intergenic spacer region.
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/db_xref="taxon:74884"
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/organelle∞"plastid:chloroplast"
/db_xref∞"taxon:74887"
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Chloroplast Dryadodaphne sp. Gray 4853
Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; Laurales; Monimiaceae; [1]
(bases 1 to 657)
Renner, S.S.
   Doryphora aromatica.
Chloroplast Doryphora aromatica
                                                                  Doryphora aromatica sequence. AF198494
                                                      AF198494.1
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/db_xref-"taxon:106839"
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/note-"trnT-trnL intergenic spacer region"
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Spermatophyta;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATGATAGAATCATTTCTGATTGGA 509
                                                                                                                                    Direct Submission
Submitted (14-FEB-1999) Biology, Univ. of Missouri-St. Louis, Natrual Bridge Rd., St. Louis, MO 63121, USA
Location/Qualifiers
                                                                                                                                                                                                                                         Circumscription and phylogeny of the Laurales: evidence from molecular and morphological data Am. J. Bot. (1999) In press

2 (bases 1 to 668)
                                                                                                                                                                                                                                                                                                                                                        Daphnandra repandula.
Chloroplast Daphnandra repandula
Eukaryota, Viridiplantae; Embryop
Magnoliophyta; Laurales; Monimiao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF129022 668 bp DNA PLN 17-MAR-199 Daphnandra repandula chloroplast trnT-trnL intergenic spacer
                                                                                                                                                                                                                                                                                                                        Renner, S.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF129022.1 GI:4427014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Renner, S.S., Foreman, D.B. and Murray, D. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Syst. Biol.
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1 (bases 1 to 657)
Renner, S.S., Foreman, D.B. and Murray, D.
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                                                                                                                                                                                                                                                                                                                                            (bases
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3.389
72.000
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81 c 126 g 187 t
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/organelle="plastid:chloroplast"
/db_xref="taxon:49996"
             /note="trnT-trnL intergenic spacer region"
84 c 127 g 195 t
                                                     /db_xref="taxon:74883"
1. .668
                                                                                       /organism="Daphnandra repandula"
/organelle="plastid:chloroplast"
                                                                                                                                                                                                                                                                                                                                        1 to 668)
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                                                                                                                                  . 668
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                                                                                                                                                                                                                                                                                                                                                          Monimiaceae;
                                                                                                                                                                                                                                                                                                                                                                            Embryophyta;
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6
                                                                                                                                                                                                                                                                                                                                                            Daphnandra
                                                                                                                                                                                                                                                                                                                                                                              Tracheophyta; Spermatophyta;
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REFERENCE
AUTHORS
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ORGANISM
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VERSION
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                                                                                                                                                                                                                                                                                                                                     requests: clonerequest/sampler.ac.uk
On Feb 5, 2001 this sequence version replaced gi:12214260.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated repeat sequence elements. Where the sequence is
ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em; EmBL; Swy. SWISSPROT; Tr; TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/Projects/Chre6
Poleter de Jong. For further details see
http://www.sanger.ac.uk/Projects/Onme.htm
                                                                                                                           once, except for a 100 base overlap.
The true left end of clone RP1-83M4 is at 1 in this sequence. The true left end of clone RP1-91J24 is at 104129 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human DNA sequence from clone RP1-83M4 on chromosome
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                                                                                                                                                                                                               IMPORTANT: This sequence is not the entire insert of clone RP1-83M4
It may be shorter because we sequence overlapping sections only
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Bagguley,C.
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                                                                                                                                                                                                                                                                                         VECTOR: PCYPAC
                                                                                                                                                                                                                                                                                                                       http://www.chori.org/bacpac/home.htm
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3.389
72.000
                                                                                                 Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Eutheria; Primates;
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/clone~"RP1-83M4"
/clone_lib="RPCI-1"
1302. .1605
                                                                                                                                                                                                                                                                         /note-"30 copies 2 mer cc 68% conserved"
15931. .16276
/note-"1199ger4(Zombi) repeat: matches 2383. .2731 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L2 repeat: matches 2609.
8707. .8977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="AluSp repeat: matches 1. .278 of consensus"
5613. .5697
                                                                                                          /note-"Sequence from overlapping clone bA3B11 (AL512354).
Assembly confirmed by restriction digest."
18383. 18643
                                                                                                                                                                                 /note="Tigger4(Zombi) repeat: matches 627.
                                                                                                                                                                                                                                                                                                                                                  /note="MIR repeat: matches 70. .212 of consensus" 15188. .15497
/note="All&x repeat: matches 1. .311 of consensus" 15498. .1557
                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSp repeat: matches 1. .313 of consensus"
14484. .14623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MIR repeat: matches 202.
2581. .2634
   'note="MIR repeat: matches 154. .258 of consensus"
20848. .20937
                                     note="Tigger4(Zombi) repeat: matches 1.
9527. .19632
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSq repeat: matches 1. .310 of consensus"
l3845. .14157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="L2 repeat: matches 2596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSx repeat: matches 1. .268 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /197. .7476
/note="2 copies 140 mer 85% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note¤"LTR16A repeat: matches 169. .450 of consensus"
5681. .6805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluSx repeat: matches 1.
2223. .2533
                                                                                                                                                                      .6997. .17123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note⇔"FLAM_C repeat: matches 1.
2102. .12143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MIR repeat: matches 65. .150 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .966. .4024
'note="AluJ/FLAM repeat: matches 35. .77 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="L2 repeat: matches 1866. .2190 of consensus"
1573. .2617
                                                                                         note="AluJo repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note-"AluJo repeat: matches 142.
2648. .12786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note-"L2 repeat: matches 2355. .2530 of consensus"
                                                                                                                                                                                                                     note-"AluJb repeat:
6588. .18382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note-"AluSx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="AluJo repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="AluSx repeat: matches 1. .301 of consensus"
1963. .12086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MIR repeat: matches 1. .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .7704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .7962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .12456
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                                                                                                                                                                                                                                                            .16587
                                                                                           matches 7.
                                                                                                                                                                                                                                        matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     matches 1. .304 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matches 98.
                                                                                                                                                                                                                                        6. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2745 of
                                                                                         .275 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .142 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .282 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .124 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         consensus"
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                                                        .627 of consensus"
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20940. .21242
/note-"MITH repeat: matches 70.
22808. .23017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="THEIA repeat: matches 1. 29985. .30289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSx repeat: matches 1. .195 of consensus 25005. .25087 /note="MIR repeat: matches 92. .185 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23035. .23336
/note="AluJb repeat:
23523. .23658
                                                                                                          /note="44 copies 2
42592. .42760
                                                                                                                                              /note="23 copies 4 mer ttct 75% conserved"
42501. .42588
                                                                                                                                                                                                                                                                                              /note="L1MB2 repeat: matches 6099. .6167 of consensus"
41558. .41965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"AluY repeat: matches 1. .311 of consensus"
37710. .37993
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   /note≔"AluSq
15830. .46141
                                   /note="Alusx repeat: matches 1.
15082. .45396
                                                                         /note="FRAM repeat:
13997. .44315
                                                                                                                                                                                   12500. .42591
                                                                                                                                                                                                    /note-"L2 repeat: matches 2172.
                                                                                                                                                                                                                     2352. .42498
                                                                                                                                                                                                                                        /note-- "L1MB2 repeat: matches 5705.
                                                                                                                                                                                                                                                                                                                                                 'note="L2 repeat: matches 2007. .2143 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                    'note="L2 repeat: matches 1806.
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note⇔"AluSx repeat: matches 1.
11221. .41256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MIR repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
}7387. .37697
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35362. .36232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="23 copies 2 mer tt 76% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note-"MIR repeat: matches 71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"MER5A repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluSx repeat: matches 1.
30313. .30457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="THE1B repeat: matches 1.
29032. .29383
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23659. .23917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="CpG island"
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                                                                                                                                                                                                                                                                           note-"MSTA repeat: matches 1. .426 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                      note="18 copies 2 mer ac 100% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note-"L1PA7
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                  repeat: matches 1.
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                                                                                                                             mer tt 73% conserved'
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                                                        .309 of
                                                                                         .176 of
                                                                                                                                                                                                    .2318 of consensus"
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                    .313 of consensus
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Quality:
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ORGANISM
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MEDLINE
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                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (12-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                Submitted (13-OCT-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Oct 13, 2000 this sequence version replaced gi:7230340. Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                              Erratum:[[published errata appear in Science 1999 Jan
1;283(5398):35 and 1999 Mar 26;283(5410):2103 and 1999 Sep
3;285(5433):1493]]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 132558)
The C. elegans Genome Sequencing Consortium, Washington University Genome Sequencing Center, St. Louis U.S.A. and the Sanger Centre,
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                                                                                                                                                                                                                                          Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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                                                                                                                                                                                                                    Submission
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/note="THEIC repeat: matches 1. .371 of consensus" 47562. 47629
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                Genome Sequencing Center
Department of Genetics, Washington
St. Louis, MO 63110, USA, and
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77.273
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Gaps: 0
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                                                                                                                                                                                                                                                                                                      Louis,
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NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted:

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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_htg15:AC069263
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US-09-251-133-6 x AC025716
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ORIGIN
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LOCUS Arnkarer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AC025716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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Muzny, D.M., Addans, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Bentcon, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Bieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Eurich, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, S., Chowlbry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, M., Gunaratte, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Haylak, P., Hade, S., Hollins, B., Homsi, F., Howard, S., Huber, J., Hullyk, S., Hume, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, W., Loulse, R., Luna, R., Mastinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mela, A., Mantinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mantinez, E., Massey, E., Mawhiney, E., Mitchell, T., Mohabbat, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGCCGACTAGGTGAAGGTTCTCCCATTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG 10-NOV-20, Homo sapiens chromosome 12 clone RP11-592B21, WORKING DRAFT SEQUENCE, 11 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 156768)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC069263.8 GI:11128186
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3.389
66.667
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/db_xref="taxon:6239"
/chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Caenorhabditis elegans"
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Gaps: 0
Percent Identity: 48.148
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JOURNAL REFERENCE

TITLE

AUTHORS TITLE JOURNAL

COMMENT

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Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, N., Nguyen, N., Nguyen, N., Nickerson, E., Nwokankwo, S., Nguyen, N., Oyiedo, R., Pace, A., Payton, B., Oyiedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Ouiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoshitari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 9, 2000 this sequence version replaced g1:9966656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nov 9, 2000 this sequence version replaced gi:9966656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye-primer Bodipy: 74% of reads Chemistry: Dye-terminator Big Dye: 26% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 148444 bases at least Q40 Consensus quality: 153372 bases at least Q30 Consensus quality: 153466 bases at least Q30 Consensus quality: 155446 bases at least Q30 Consensus quality: 155446 bases at least Q30 Consensus quality: 155446 bases; agarose-fp estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation
                                                           136098
136198
143819
143919
143919
149745
149845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                     53910
54010
81913
82013
98593
98693
113383
113483
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                                                                                                                                                                                                                                                               125819
125919
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                                                                                            143818:
143918:
149744:
149844:
152407:
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113382:
                                                                                                                                                                                                                                 125818:
125918:
136097:
136197:
                                                                                                                                                                                                                                                                                                                                                                                                                                   53909: contig of 53909 bp in length
54009: gap of unknown length
81912: contig of 27903 bp in length
82012: gap of unknown length
98592: contig of 16580 bp in length
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                                                                                                                                                                                           2: contig of 27903 bp in length
2: gap of unknown length
2: contig of 16580 bp in length
2: gap of unknown length
2: contig of 14690 bp in length
2: gap of unknown length
2: gap of unknown length
3: contig of 12336 bp in length
4: contig of 10179 bp in length
7: gap of unknown length
7: gap of unknown length
8: contig of 7621 bp in length
8: contig of 7621 bp in length
3: gap of unknown length
1: contig of 5826 bp in length
4: gap of unknown length
7: contig of 2563 bp in length
7: gap of unknown length
7: gap of unknown length
7: gap of unknown length
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REFERENCE
AUTHORS
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ORGANISM
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: AC069263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-251-133-6 x AC069263/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151959 TGGATTGCTTGAGCCTCTGAGT 151938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
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                                                                                                                                                  Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 144239 bases at least Q30
Consensus quality: 150252 bases at least Q30
Consensus quality: 150252 bases at least Q20
Insert size: 206767; 2.8% error; agarose-fp
Quality coverage: 2.85x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL356986 161082 bp DNA
Homo sapiens chromosome 1 clone RP
PROGRESS ***, 33 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (14-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
* NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                       Center project name: bA395N6
                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Jan 22, 2001 this sequence version replaced gi:9797641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plumb, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 161082)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                             coverage: 2.53x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
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/db_xrefo"taxon:9606"
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Location/Qualifiers
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1 clone RP11-395N6, *** SEQUENCING
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of N, but the exact sizes of the gaps are unknown

/organ.sm=".4omo saptens" /db_xref="taxon:9606" /chromosome="1"	urce 1161082	0 161082; contig of 269;	0 158289: contig of 0 158389: gap of	tig of f	151847: contig of 2 151947: gap of	149102: contig of 149202: gap of	* 133409 142799; contig of 9391.bp in length * 142800 142899; gap of 100 bp	133308: contig of 133408: gap of	129730; contig of a 129830; gap of	* 118214 124762; contig of 6549 bp in length * 124763 124862; gap of 100 bp	118113: contig of ;	H	104990: contig of 3944 bp in 1 105090: gap of 100 bp	101046: gap of 100 bp	96990: gap of 100 bp	93224: gap of 100 bp	* 90316 93124; contig of 2809 bp in length	90215: contig o	87894: contig of	85549: contig of 85649: gap of	82107: contig o 82207: gap of	78134: gap of	13636 pp 10	61599: gap of 100 bp	42733: gap of 100 bp 61499: contiq of 18766 bp in	42633: contig of	38178: contig of	33337: contig of	30221: contig o	24722: contig o: 24822: gap of	20121: contig 20221: gap of	17004: gap of 100 bp	of 100 bp	11008: gap of 1000 bp 11	8362: gap of 100 bp	of 100 bp in	preserved. 1 5857: contig of 5857 bp	
misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature		misc_feature			misc_reacure		misc_feature		misc_feature	misc_reature		misc_feature		misc_feature	ייידפר דבמרמדם		misc_feature		misc_feature	misc_reacure		misc_feature		misc feature	misc_feature	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-251-133-6
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ID AAZ46827 standard; cDNA; 1506
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CC polynucleotides encoding the proteins. The polypeptides are useful for cc modulating the expression of human RNA binding proteins (RNABP) which cc play a role in cancer, immune disorders and developmental disorders. CC Disorders associated with a decrease of RNABP include: cancers such as cc adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, cc teratocarcinoma, and, in particular, cancers of the adrenal gland, cc bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, cc gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, cc pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, cc testis, thymus, thyroid, and uterus, immune disorders such as acquired communodeficiency syndrome (AIDS), Addison's disease, adult respiratory cc distress syndrome, allergies, ankylosing spondylitis, amylodosis, cc anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune cthyroiditis, bronchitis, cholecystitis, contact dermatitis, crohn's cc disease, atopic dermatitis, dermatomyositis, diabetes mellitus, cc emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis cc emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis condpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hyporesis, pancreatitis, polympositis, psoriasis, cc myasthenia gravis, myocardial or perioardial inflammation, customic, sundrome, rheumatoid arthritis, sclaroderma, Sjogren's customic, arabhylavis excetemic lymphoperators customic, suctomic, su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders and developmental disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated and purified polynucleotide for modulating the human RNA binding proteins which play a role in cancer,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA binding protein; RNABP; cancer; immune disorder; AIDS; human; developmental disorder; acquired immunodeficiency syndrome; RNABF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human RNA binding protein (RNABP)-2 encoding cDNA (clone 1250374).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides human RNA binding proteins (RNABP) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Examples; Columns 51-52; 39pp; English.
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systemic anaphylaxis,

erythematosus, systemic

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seq_documentation_block:
ID AAD00552 standard; DNA; 20966 BP.

XX AC AAD00552;

XX DT 29-AUG-2000 (first entry)

XX DE Human APM1 (Adipose Most Abundant Gene Tr

KW APM1; Adipose Most Abundant Gene Tr

KW 11pid metabolism; biallelic marker;

KW atherosclerosis; insulin resistance

KW diabetes type II; linkage study; sc

XX COS Homo sapiens.

ET Location/Qualifiers

FT 5'UTR 1.4811

FT /note- "Contains th

FT /note- "Contains th

FT /number- 1

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US-09-251-133-6 x AAZ46827/rev
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary uncoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibiromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Syndenham's chorea and cerebral palsy, spina bifida, anencephaly, crantorachischisis, congenital glaucoma, cataract, sensorineural bearing loss, and any disorder associated with cell growth and differentiation, embryogenesis, and morphogenesis involving any tissue, organ, or system of a subject, e.g., the brain, advanal gland, kidney, skeletal or reproductive system. The present sequence represents a cDNA encoding the RNABP-2 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, trauma, X-linked agammaglobinemia of Bruton, common variable immunodeficiency (CVI), Digeorge's syndrome (thymic hypoplasia), thymic dysplasia, isolated immunoglobulin (Ig)-A deficiency, severe combined immunodeficiency disease (SCID), immunodeficiency with thrombocytopenia and eczema (Wiskott-Aldrich syndrome), Chediak-Higashi syndrome, chronic granulomatous diseases, hereditary angioneurotic edema, and immunodeficiency associated with Cushing's disease; and developmental disorders such as renal tubular acidosis, anemia, Cushing's syndrome,
                                                                                                                                                                                                                            APMI; Adipose Most Abundant Gene Transcript 1; human; chromosome 3p27; lipid metabolism; biallelic marker; BM; diagnosis; treatment; obesity; atherosclerosis; insulin resistance; hypertension; microangiopathy; diabetes type II; linkage study; screening; modulator; gene therapy; d
                                                                                                                                                                                                                                                                                                                     Human APM1 (Adipose Most Abundant Gene Transcript 1) genomic sequence
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/notes "Contains the promoter site"
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/bound_moiety= "Primer B5"
/note= "Amplification of amplicon 9-30"
5008..5027
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/*tag: h
/*tag: h
/*note: "The ambiguity codes in this sequence represent
polymorphic sites Al-A7 respectively, i.e. they are G,
A, T, T, G, A, G in allele 1, and C, C, C, G, T, G, A allele 2"
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/*tage g
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15144..15365
/*tag d
/number 2
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/notea "Amplicon
4599..4618
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4599..5027
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/note= "Amplification of a
4223..4642
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/bound_molety- "Primer B3"
/note- "Amplification of ar
4584.4602
/*tag- r
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/note: "Amplicon 99-14402"
/155..4175
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/*tage m
/note= "Amplicon 9-28"
3892..3911
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/notes "Amplicon 9-27"
3528..3545
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/note= "Amplification of amplicon 9-29"
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/note~ "Amplification of a
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/note= "Amplicon 9-29"
4223..4242
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/note= "Amplification of ar
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/note~ "Amplification of amplicon 9-28"
1155.,4602
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/note= "Amplification of a
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/note= "Deletion of 1 base,
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/note= "Amplification of am
/16191..16211
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/note= "Amplification of amplicon
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                     /bound_moiety= "Primer C11"
/note= "Amplification of amplicon 9-14"
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/bound_moiety= "Primer Bll"
/note= "Amplification of am
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/note= "Amplification c
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15532..15551
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15131..15150
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15131..15551
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15073..15520
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16233..16251
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/note= "Amplification of am
16233..16652
                                                                                                                                                                                                                                                                                                            /bound_moiety= "Primer B8"
/note= "Amplification of amplicon 9-12"
15503..15520
                                                                                                                                                                                                                                                                                                                                          /note- "Amplicon 9-12"
15073..15092
                                                                                                                                                                                                                                                                                                                                                                                              /bound_moiety= "Primer B7"
/note= "Amplification of a
12946..12966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "Amplicon 99-14387"
10990..11008
                                                   16633..16652
                                                                                                                                                                   /note= "Amplicon 99-14405"
15759..15776
                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "Amplicon 99-14389"
12472..12491
                                                                          '*tag=
    "Amplicon 9-15"
                                                                                                                                                                                              ; c9"
                                                           amplicon
                                                                                                                amplicon 99-14405'
                                                                                                                                             amplicon
                                                                                                                                                                                                  amplicon
                                                                                                                                                                                                                                amplicon 9-13"
                                                                                                                                                                                                                                                                                                                                                                         amplicon 99-14389
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                                                            9-14"
                                                                                                                                              99-14405
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seq_documentation_block:
ID AAZ23902 standard; DNA; 49999 BP
XX
AC AAZ23902;
XX
DT 25-JAN-2000 (first entry)
XX
DE Human LOBO homologue genomic DNA
XX
KW LOBO; long bones; bone developme
KW diagnostic; pharmaceutical; gene
KW spondyloepiphysal dysplasia; ach
XX
OS Homo sapiens.
XX
PN WO9950284-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-EP02055.
XX
PR 27-MAR-1998; 98DE-1013799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-251-133-6 x AAD00552/rev
                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ23902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                         6908 CTTTTGGGAGGCTGAGGTGGGAGCCCA 6872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6958 ANAGTTTGTCCCTACAGCCACCTTAAAAAGAGCAAGCATATAATCCCAGC 6909
                                                                                                                                                                     LOBO; long bones; bone development; bone extension; skull; osteopathic; diagnostic; pharmaceutical; gene therapy; transgenic animal; disease; spondyloepiphysal dysplasia; achondroplasia; human; ds.
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                                                                                                                                                                                                                                        Human LOBO homologue genomic DNA fragment 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
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/note= "Amplification of amplicon
17300..17503
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2.800
68.966
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17498..17517
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/note= "Amplification of
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16982..17001
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/note= "Amplification
17006..17025
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7216..17233
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Percent Identity:
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of am
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of amplicon
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of amplicon
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41.379
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seq_documentation_block:
ID AAV40370 standard; DN
XX
AC AAV40370;
XX
DT 07-DEC-1998 (first 6
XX Filamentous haemagglt
XX
DT 11-Aumentous haemagglt
XX
Filamentous haemagglt
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US-09-251-133-6
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: AAZ23902 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41460 TCTTGTATTTTTTTATAGAGATGGGGTTTTGCCCATGTTGCCCAGGCTTA 41411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel nucleic acids (I; designated LOBO (long bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. development), with exception of the skull and have osteopathic activity. The nucleic acid molecules, proteins and antibodies can be used in diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods and nucleic acid molecules, etc. are useful for production of transgenic animals, especially a transgenic mouse for the study of diseases associated with bone development, e.g. spondyloepiphysal dysplasia and achondroplasia. This sequence encodes a human LOBO protein described
                                                                                                                                                                                                                                                                                                                                                                                                          Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Filamentous haemagglutinin fragment 7 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Filamentous haemagglutinin; FHA; endothelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding proteins which influence bone development, useful for treating and studying bone disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 49999 BP; 12459 A; 12933 C; 12356 G; 12251 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 300-328; 391pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ROSE/) ROSENTHAL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                         94US-0348353.
91US-0695613.
92WO-US03725.
94US-0247572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               meningitis; therapy;
                                                                                                                                                                                                                 91US-0695613
             95US-0465929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.00
3.000
64.286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 blood-brain barrier; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
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Gaps:
Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           whooping
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1
35.714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cough; vaccine;
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6
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seq_documentation_block:
ID AAZ30127 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1875 GCTCTTGGCCATGACCTCGGCCCCGGTCTCGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1925 ACCTGCATCTTGCCCGCGTTGCGCGCGCGCCCCGGAAGTCGTCAGCGTGGC 1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pertussis filamentous haemagglutinin (FHA). Fragment 7 includes the RCD tripeptide that corresponds to amino acid residues 1097-1099 of FHA, and a carbohydrate recognition site corresponding to amino acid residues 1141-1279 of FHA. Truncated FHAs (see AAM6595) which delete the RGD region can be produced genetically and are useful as vaccines against whooping cough. The invention also provides peptides and antibodies which inhibit the reaction between the RGD tripeptide of FHA and the integrin receptors of endothelial cells and their utility as therapeutic agents, as well as a method of increasing the permeability of the blood-brain barrier using an
                                                                                                                                                                                       Filamentous hemagglutinin; FHA; Factor X; leukocyte; blood vessel endothellal cell; migration; inflamed tissue; non-fimbrial surface associated protein; Bordetella pertussis; C3bi; RGD tripeptide; integrin receptor; inflammation; antibiotic therapy;
                                                                                                                    Bordetella pertussis
                                                                                                                                                                                                                                                                            Nucleic acid encoding fragment 7 of filamentous hemagglutinin.
                                                                                                                                                                                                                                                                                                                                                                                     AAZ30127 standard; DNA;
                                                                                                                                                      autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3744 BP; 741 A; 1157 C; 1328 G; 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody to the FHA RGD region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This DNA sequence codes for 'fragment 7' (see AAW69594)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Increasing blood-brain barrier permeability - with antibody filamentous haemagglutinin RGD regions
                                                                                                                                                                        infection;
                                                                                                                                                                                                                                                                                                                26-JAN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                      meningitis; septic arthritis; endophathalmitis; disease; ss.
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                              /note- "partial sequence"
                                               /*tag-
                                                                                 Location/Qualifiers
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2.625
71.429
                                                                                                                                                                                                                                                                                                                                                                                     3744 BP
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Gaps:
Percent Identity:
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46.429
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US5968512-A.

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seq_documentation_block:
ID AAX86180 standard; DN
XX
AC AAX86180;
XX
DT 22-SEP-1999 (first e
XX
DE DNA encoding fragment
XX
KW Adhesion; leukocyte;
KW RGD region; cerebral
                                                                                                                                                                                                                           seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-251-133-6 x AAZ30127/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
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                                                                                                                                                                                                                                                               1875
                                                                                                                                                                                                                                                                                                                             1925 ACCTGCATCTTGCCCGCGTTGCGCGCGCGCGCCCGGAAGTCGTCAGCGTGGC 1876
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04-MAY-1992;
03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FHA). FHA is a non-fimbrial surface associated protein.

As there are four regions in FHA with sequence similarity to three regions in Factor X, some antibodies to these four regions cross-react with Factor X, and vice versa. The specification describes FHA peptides which interact with leukocytes or with blood vessel endothelial cells, thereby inhibiting the migration of leukocytes from the blood steam into inflamed tissue. FHA peptides competitively inhibit binding of Factor X and C3bi to leukocytes. Specifically, the peptides inhibit the reaction between the RGD tripeptide of FHA and the integrin receptors of endothelial cells. The FHA peptides (and antibodies to them) dampen inflammation during the course of therapy with antibiotics and are therefore useful in the treatment of infections e.g. meningitis, septic arthritis, and endophathalmitis, and inflammation arising from autoimmune
Adhesion; leukocyte; endothelial cell; bacteria; Bordetella pertussis; cilliated respiratory epithelial cell; filamentous haemagglutinin; FHP RGD region; cerebral endothelial cell; inflammation; antibiotic therap
                                                                   DNA encoding fragment 7 of the filamentous haemagglutinin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encoues (FHA). FHA is a non-fimbrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides inhibiting the influx of leukocytes into inflamed tissue, useful for dampening inflammation during treatment with antibiotics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 10A-L; 81pp;
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                                                                                                                                                                                                                         /SIDS8/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX86180
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                                                                                                     (first entry)
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92WO-US03725.
91US-0695613.
94US-0247572.
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Gaps:
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filamentous haemagglutinin; FHA;
inflammation; antibiotic therapy;
                                                                                                                                                                                                                                                               1842
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46.429
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alignment_scores:
Quality:
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                                                                                                                                                                     1875
                                                                                                                                                                                                                              1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The specification describes peptides which inhibit adhesion between leukocytes and endothelial cells, and peptides which inhibit adhesion between bacteria (Bordetella pertussis) and cilliated respiratory epithelial cells. The specification also describes an immunogenic composition comprising a polypeptide portion of Bordetella pertussis filamentous haemagglutinin (PHA) containing no RGD region or containing an amino acid sequence altered in the RGD region, where the polypeptide portion elicits antibodies which do not cross-react with cerebral endothelial cells. The peptides and methods are useful for reducing inflammation during the course of antibiotic therapy of infectious diseases such as meningitis, septic arthitis, and endophathalmitis. The present sequence encodes fragment 7 of the FHA protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-NOV-1994;
03-MAY-1991;
04-MAY-1992;
           FHA fragment 7 polypeptide encoding
                                        30-MAY-2000
                                                                                               AAZ57049 standard; DNA; 3744
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3744 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides inhibiting the adhesion between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-443571/37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection; meningitis; septic arthritis; endophathalmitis; ss.
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                                                                                                                                                                     nLeuLeuGlyLeuLeuSer...ProValSerLeu
                                                                                                                                                                                                                             ACCTGCATCTTGCCCGCGTTGCGCGCGCGCGCCCGGAAGTCGTCAGCGTGGC 1876
                                                                                                                                                                                                                                                      ThrCysValLeuGlyTyrLeuHisIleValProGluPheIleGluSerGl 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for treating inflammation
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                                      (first entry)
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91US-0695613.
92WO-US03725.
94US-0247572.
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2.625
71.429
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Gaps: 1
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seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA10263
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US-09-251-133-6 x AAZ57049/rev
                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC The invention provides a novel pharmaceutical composition for increasing CC the permeability of the blood-brain barrier to a molecule (I). The CC composition comprises (I) and an antibody to FHA (filamentous hemagylutinin) which binds to endothelial cells in brain blood vessels, CC increasing permeability. FHA contains polypeptide regions with binding CC properties similar to those of complement C3bi, factor X and integrin CC receptor CR3, and some anti-FHA antibodies are competitive inhibitors CC of these materials, i.e. they reduce leukocyte migration or bacterial adhesion. The compositions are used to improve delivery of (I) to the brain, e.g. where (I) is used to treat brain cancer, acquired immune CC brain, e.g. where (I) is used to treat brain cancer's diseases or other neurological diseases. Other antibodies directed against particular CC regions of FHA are used to treat inflammation (caused by microbial CC regions of FHA are used to treat inflammation (caused by microbial CC regions of FHA are used to treat inflammation of Bordetella CC represents a FHA fragment 7 encoding gene.
                                                                                                                                                                                                                         Align seg 1/1
                                                                                                                                                 1925 ACCTGCATCTTGCCCGCGTTGCGCGCGCGCGCGGAAGTCGTCAGCGTGGC 1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-NOV-1994;
04-MAY-1992;
03-MAY-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Compositions containing antibody to filamentous hemagglutinin, e.g. to increase permeability of the blood-brain barrier and tinflammation or bacterial adhesion \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Masure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-inflammatory; anticancer; antiviral; antineurodegeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FHA; blood-brain barrier; filamentous hemagglutinin; endothelial cell; complement C3bl; factor X; integrin receptor CR3; leukocyte migration; bacterial adhesion; brain cancer; acquired immune deficiency syddrome; Parkinson's disease; Alzheimer's disease; antibacterial; anti-epileptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYRQ ) UNIV
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                                                                                                                                                                       nLeuLeuGlyLeuLeuSer...ProValSerLeu
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                                                                         GCTCTTGGCCATGACCTCGGCCCCGGTCTCGTTG 1842
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92WO-US03725.
91US-0695613.
94US-0247572.
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2.625
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alignment_block:

Ratio: Percent Similarity:

52.50 2.625 71.429

Length: 28
Gaps: 1
Percent Identity: 46.429

US-09-251-133-6 x AAA10263/rev

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alignment_scores:
Quality:
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                                                                                                                                                           This sequence represents the filamentous haemagglutinin gene, fhab, from CC Bordetella pertussis. Bordetella pertussis is a small Gram negative CC bacillus found only in humans and which causes whooping cough (pertussis) in children. Filamentous haemagglutinin (FHA) is a 368 kD surface-CC associated protein which is thought to be one of the most important CC factors in mediating the adhesion of the bacterium to a eukaryotic (human) cell. FHA also stimulates an immune response in humans following CC disease, and has been shown to act as an immune products, are used for CC animal model. The FHA gene, or its expression products, are used for CC enimal model. The FHA gene, or its expression products, are used for CC prevention or treatment of pertussis, particularly in vaccines. It may CC pertussis or other organisms. Fragments of the gene may be used as CC diagnostic hybridisation probes or as antisense modulators to reduce the CC used in immunoassays to detect anti-FHA antibodies, and to raise CC antibodies for the diagnosis, prevention of treatment of whooping cough.
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10-AUG-1992;
27-OCT-1988;
                                                                                                               Sequence 11883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Columns 11-28; 17pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella pertussis filamentous haemagglutinin gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid encoding the filamentous hemagglutinin of Bordetella pertussis, useful for diagnosis, treatment and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
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) DOMENIGHINI I
) RAPPUOLI R.
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88US-0263648
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253..11043
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                                                                                                                  A; 3648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FHA; fhaB gene;
c; immunogenic;
                                                                                                                  ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DA,
                                                                                                                  4282 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rappuoli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                whooping cough; pert
                                                                                                                  1754
                                                                                                                  Τ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fhaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pertussis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of.
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Align seg 1/1

to reverse of: AAA10263 from: 1

6

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seq_documentation_block:
ID AAQ04668 standard; DN
XX AAQ04668;
XX AAQ04668;
XX FHA STRUCTURAL gene,
XX FARS
FT -0.5 ignal 79. tag
FT RBS
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FT RBS
FT CDS 7*tag
FT CDS 7*tag
FT CDS 7*tag
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FT
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  The sequence is an EcoRI fragment contg. an ORF of 10789 bp. beginning at an ATG 253 bp from the left-hand EcoRI site. Two other in-frame ATG codons are located 45 and 174 bp after the beginning of the ORF; at approx. the position of the third ATG begins the
                                                                                                                                                                                    Nucleic acid sequences encoding and peptide cross-reactive with pertussis, useful for diagnosis
                                                                                                                                      Disclosure; ; lpp; English.
                                                                                                                                                                                                                                                                                               WPI; 1990-164024/21.
P-PSDB; AAR05041.
                                                                                                                                                                                                                                                                                                                                                                                                                             (STRD ) LELAND STANFORD JUNIOUR UNIVERSITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FHA structural gene, fhab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nLeuLeuGlyLeuLeuSer...ProValSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCTGCATCTTGCCCCGCGTTGCGCGCGCGCCCCGGAAGTCGTCAGCGTGGC 4711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrCysValLeuGlyTyrLeuHisIleValProGluPheIleGluSerGl
                                                                                                                                                                                                                                                                                                                                                                            Domenighini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haemagglutinin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88US-0263648; WO-U04732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89WO-US04732
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/label=fhaB
1468..1746
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253..1348
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/*tag= g
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159..162
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/label-A
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111..117
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'note=" ABABA "
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                                                                                                                                                                                                                                                                                                                                                                            ĭ
                                                                                                                                                                                                                                                                                                                                                                         Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fhaB; whooping cough; vaccine;
                                                                                                                                                                                    Bordetella pertussis fham gene filamentous haemagglutinin of b and treatment of whooping cough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
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                                                                                                                                                                                                                                                                                                                                                                            Falkow S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
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alignment_block:
    US-09-251-133-6 x AAQ04668/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4710 GCTCTTGGCCATGACCTCGGCCCCGGTCTCGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4760 ACCTGCATCTTGCCCGCGTTGCGCGCGCGCCCCGGAAGTCGTCAGCGTGGC 4711
This sequence encodes a human protein kinase C inhibitor (designated IPKC-1) initially identified among the partial CDNAs (Incyte clones shown in AAT76789-93) from a THP-1 library (THPIPEB01). IPKC may be useful for diminishing multiple drug resistance in cancer chemotherapy, for treating melanomas or other cancers, for treating autoimmune diseas
                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use of codons strongly preferred by B pertussis. The relative GC content of the ORF is 67.5%. The DNA and recombinant peptides produced from it are useful diagnostically and therapeutically against pertussis. Dosage is pref. 25-75 microg/kg (single dose)
                                                                                                                      DNA encoding protein kinase C inhibitor polypeptide - useful diminishing multiple drug resistance in cancer chemotherapy
                                                                                                                                                                                                                                                                              18-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic assay; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; protein kinase C inhibitor; IPKC-1; multiple drug resistance; cancer chemotherapy; autoimmune disease; inhibit; memory decline; Alzheimer's disease; screen; agonist; antagonist; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein kinase C inhibitor, IPKC-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT76788 standard; cDNA;
                                                                                              Claim
                                                                                                                                                                                      WPI; 1997-372057/34.
                                                                                                                                                                                                                 Au-Young J,
                                                                                                                                                                                                                                               (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                            18-JUN-1996;
                                                                                                                                                                                                                                                                                                                                          15-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                         US5648238-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ThrCysValLeuGlyTyrLeuHisIleValProGluPheIleGluSerGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nLeuLeuGlyLeuLeuSer...ProValSerLeu 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                           2; Column 31-32; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                       AAW18878
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                                                                                                                                                                                                                    Hawkins
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254..642
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2.625
71.429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    640 BP
                                                                                                                                                                                                                   Hillman JL;
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Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coding sequence
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for treating autoimmune diseases

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ពិត្តត្តត្តត្តត្ត
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                                                                                                                                                                                                                                                                                                                                                                                                             IPKC; human protein kinase C inhibitor polypeptide; multiple sclerosis; protein kinase C; multiple drug resistance; lymphoma; breast cancer; intestinal cancer; auto-immune disorder; Alzheimer's disease; memory disorder; rheumatoid arthritis; myasthesia gravis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or to inhibit memory decline in Alzheimer's disease, or to screen for therapeutic IPKC agonists, antagonists or inhibitors. The nucleic acid sequence, oligonucleotides and antiseas equences derived from the IPKC-1 coding sequence or the Incyte clones can also be used in diagnostic assays of body fluids or biopsied tissues to detect the expression level of IPKC-1, or to monitor modulation of the transcripts
  Disclosure; Fig 1A-B;
                                           New human protein kinase C inhibitor polypeptide - treatment of diseases associated with action of pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein kinase C inhibitor homolog (IPKC) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 640 BP;
                                                                                                                                                         (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV34636 standard; cDNA; 640 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 rGlnLeuLeuGly 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ArgThrCysValLeuGlyTyrLeuHisIleValProGluPheIleGluSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGCTCCTCGGA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGAGTTGCCTGCGCCCTTGGCCACTTCATTCCTCATCAGTCACACCT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to reverse of: AAT76788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                               Hawkins PR,
                                                                                                                                                                                     96US-0666798
97US-0892692
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                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 254..639
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3.188
76.190
                                                                                                                                                                                                                                                                                                                /product= "IPKC polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 A; 189 C;
                                resistance
  28pp; English
                                                                                                                               Hillman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
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Gaps:
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47.619
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                                           protein
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*3333333333×3
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                                                                                                                      seq_documentation_block:
ID     AAX21440 standard;
XX
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US-09-251-133-6 x AAV34636/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: AAV34636
                                                                                                                                   18-JUN-1996;
14-JUL-1997;
11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                        Human; protein kinase C inhibitor; IPKC; homologue; diagnosis; tumour; multidrug resistance; chemotherapy; cancer; apoptosis; lymphoma; ss; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; breast; myasthenia gravis; intestine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This cDNA encodes a human protein kinase C inhibitor polypeptide homolog (IPKC). IPKC and compositions containing IPKC are useful for treating diseases and conditions associated with protein kinase C, such as multiple drug resistance, cancer, especially lymphoma, intestinal and breast cancer, memory disorders, as observed in sufferers of Alzheimer's disease, and auto-immune disorders such as rheumatoid arthritis, multiple sclerosis and myasthesia gravis. IPKC is more selective in its mode of inhibition, and has less risks associated with toxicity compared with
Detecting polynucleotides encoding protein kinase C inhibitor
                                                                                                                                                                                                                             09-MAR-1999
                                                                                                                                                                                                                                                           US5879893-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 AGGAGTTGCCTGCTGGCCTTGGCCACTTCATTCCTCATCAGTCACACCT 243
                               P-PSDB; AAW78495.
                                              WPI; 1999-203946/17
                                                                                                                                                                                                11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein kinase C inhibitor homologue gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX21440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 640 BP; 122 A; 189 C;
                                                                                                       (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      previous synthetic inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 rGlnLeuLeuGly 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgThrCysValLeuGlyTyrLeuHisIleValProGluPheIleGluSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGCTCCTCGGA
                                                                                                                                                                                                                                                                                                                                                                 sapiens
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                                                                           Hawkins
                                                                                                                                   96US-0666798.
97US-0892672.
98US-0096071.
                                                                                                                                                                                                98US-0096071
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 256..642
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3.188
76.190
                                                                                                                                                                                                                                                                                      /*tag= a
/product= "Protein kinase C inhibitor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA; 642
                                                                            PR,
                                                                            Hillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
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47.619
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US-09-251-133-6 x AAX21440/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represent the cDNA containing the coding region for a human protein kinase C inhibitor (IPKC) homologue. The IPKC gene can be used in the diagnosis, study, prevention and treatment of disease associated with PKC, e.g. to diminish multidrug resistance while maintaining the sensitivity of tumor cells to chemotherapy, for treating cancers, to induce apoptosis, e.g. in autoimmune disorders such as rheumatoid arthritis, multiple sclerosis, and myasthenia gravis, and
                                                                                                                                                                                                                                                                                                                              Transcription factor; seed storage protein; lectin; oil-body protein; Pv-Seed factor-1; ROM1; Vicilin-box binding protein-1; ROM2; 7S-globulin; phaseolin; PHA-L; bean; nuclear protein; promoter; PCR primer; bZIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               using an oligonucleotide probe to samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of bZIP2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 GCAGCTCCTCGGA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 642 BP; 122 A; 189 C; 214 G; 115 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancers such as lymphoma, intestinal and breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 rGlnLeuLeuGly 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ArgThrCysValLeuGlyTyrLeuHisIleValProGluPheIleGluSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT:AAC84565
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                97US-0796899
                                                                                                                                                                                                      /note= "contains internal stop codons encoding residues in the corresponding protein
                                                                                                                                                   /note- "contains residues
                                                                                                                                                                                                                                                             Location/Qualifiers
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3.188
76.190
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                                                                                             internal stop codons encoding in the corresponding protein i
                                                                                                                                                 internal stop codons in the corresponding
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to:
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                                                                                                                                                 encoding
protein A
                                                                                             protein AAB48243"
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AAB48241"
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alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 _documentation_block:
                                                                                                             signal peptide containing protein; SIGP, human; cancer; immune response; adenocarcinoma; leukemia; lymphoma; melanoma; myeloma; sarcoma; AIDS; Addison's disease; adult respiratory distress syndrome; allergy; anemia; asthma; atherosclerosis; bronchitis; cholecystitus; Crohn's disease; ulcerative colitis; atopic dermatitis; dermatcomyositis; emphysema; diabetes mellitus; atrophic gastritis; glomerulonephritis; gout; trauma; drave's Disease; hypereosinophilia; irritable bowel syndrome; infection; lupus erythematosus; multiple sclerosis; myasthenia gravis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated transcription factor gene which is expressed in a recombinant maturing dicot seed and which encodes a transcription factor protein which targets a promoter of a gene encoding seed storage proteins, lectins or oil-body proteins. The transcription factors isolated are Pv-Seed factor-1 (ROM1) and Vicilin-box binding protein-1 (ROM2). These factors bind to 7S-globulin (b-phaseolin) or lectin (PHA-L) promoters. The transcription factor gene is useful for enhancing or reducing expression of seed storage protein, lectin or oil-protein genes in dicot seed crops. The present sequence represents the nucleotide sequence of bZIP2 (basic leucine zipper) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel transcription factor gene which encodes transcription factor protein that targets promoters of genes encoding seed storage protein useful for modulating seed storage protein expression in dicot
                                                                         osteoarthritis; osteoporosis; pancreatitis; polymyositis; scleroderma; rheumatoid arthritis; Sjogren's syndrome; autoimmune thyroditis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                          AAX82076 standard; DNA; 846 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 CTATTGGGCCACATTCACACGGTCAAGGAGTTCCATCCCCACCTGCTGCT
                                                                                                                                                                                                                                                                                                    Human SIGP encoding DNA (clone ID 866885).
                                                                                                                                                                                                                                                                                                                                              20-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 uGlyLeuLeu 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 ValLeuGlyTyrLeuHisIleValProGluPheIleGluSerGlnLeuLe 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-079619/09
DB; AAB48241, A
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Gaps: 0
Percent Identity: 55.000
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dicot seed
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WO9933981-A2 Homo sapiens

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seq_documentation_block:
ID AAA81477 standard; DN
XX
AC AAA81477;
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DT 04-DEC-2000 (first e
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US-09-251-133-6 x AAX82076/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC A host cell containing a vector comprising SIGP DNA can be used to produce the SIGP protein. The SIGP protein can be used, in conjuncture could be a pharmaceutical carrier to treat or prevent a cancer. An antagonist confirm the SIGP protein can be used to treat or prevent a cancer on an accountable of the SIGP protein can be used to treat or prevent a cancer or an accountable of the SIGP protein can be used to treat or prevent a cancer or an accountable of the SIGP protein can be used to treat or prevent a cancer or an accountable of the SIGP protein can be used to treated or prevented include sarcomas, adenocarcinomas, leukemia's, lymphomas, melanomas, consideration of the accountable of the accountable
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: AAX82076
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                                                                                                                                                                                                                                          434
                                                                                                                                                                                                                                                                                                                                           484 AAGGCCTGCATCCTGTTCTTGGATAATTTTCTGCTGCTGCTGCTGCCGGATTT 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human signal-peptide containing protein coding sequences used to treat cancer and immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 846 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides human signal-peptide containing proteins (SIGP) (AAX21841-855) and polynucleotides (AAX82076-90) encoding the proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 89; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-430242/36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-DEC-1997;
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                                                                                                                                                                                                                                                                                          14 eIleGluSerGlnLeuLeuGlyLeuLeu 23
                                                                                                                                                                                                                                                                                                                                                                                                1 ArgThrCysValLeu......GlyTyrLeuH1sIleValProGluPh 14
                                                                                                                                                                                                                                       CATCAAAACCCAAGCCTCTGGTCTCCTC 407
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Shah P;
     (first entry)
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2.525
76.923
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                                                                                                           DNA; 26778 BP
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alignment_block:
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CC represent specifically claimed Neisseria meningitidis genomic DNA
CC sequences; AAA81260 to AAA81303 and AAB25620 to AAB2563 represent
CC Neisseria DNA sequences and their corresponding proteins; AAA81254 to
CAAA81259 and AAA81304 to AAA81312 represent PCR primers used in the
CC CAAA81259 and AAA81304 to AAA81312 represent PCR primers used in the
CC CAAA81452 represent Neisseria meningitidis DNA sequences; and AAA81322 to
CC CAAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
CC composition. The nucleic acid sequences, protein sequences, and antibodies
CC composition can be used in the manufacture of a composition. The
CC composition can be used in the manufacture of a composition. The
CC composition can be used in the manufacture of a composition due to
CC composition can be used as a medicament (our in the manufacture of a
CC medicament) for treating, preventing or diagnosing infection due to
CC composition tall pathogenic Neissariae. Identified proteins could
CC composition apathogenic Neissariae. Identification of sequences
CC particularly organism specific probes. Attempts to make efficacious
CC particularly organism specific probes. Attempts to make efficacious
CC Multivalent vaccines have also been tried but none have successfully
CC overcome antigenic variability. The provision of further, complete
                                                            Align seg 1/1 to reverse of: AAA81477
                                                                                                      US-09-251-133-6 x AAA81477/rev
                                                                                                                                                                Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                              sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 524-531; 1760pp; English.
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Masignani V, Galeott
Rappuoli R, Pizza M;
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Meningococcus B; MenB; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N. meningitidis partial DNA sequence gnm_25 SEQ ID NO:25
                                                                                                                                                                                                                                                                                      Sequence 26778
                                                                                                                                                                                                                                                                                                                             other more variable regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-1998;
30-APR-1999;
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Quality:
Ratio:
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99US-0132068
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61.538
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Ratti G, Scarselli
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46.154
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21978 TGCTTTCTTGGTTATTAACACGTAGTAATGGAGTATCAGAAAATACATCA 21929

15 .IleGluSerGlnLeuLeuGlyLeuLeu 23 ::: |||:::|||||||||||||| 21928 CACAAAATTACAATTCCTTGGTTTGCTG 21901

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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     score q
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                                                                                                                                                                                                                                                                                                                                              Score
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     Issued_Patents_AA:*
1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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length: 2000000000
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Gapop 10.0 , Gapext 0.
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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 US-08-796-899-27
US-08-403-866-6
US-08-457-245-8
US-08-939-002A-16
US-09-382-155-20
US-09-318-514-3
US-09-115-934A-3
US-09-115-934A-3
US-08-403-634-2
US-08-913-441B-2
US-08-913-441B-2
US-09-036-987A-2
5171684-7
US-09-234-613-20
US-09-234-613-20
US-09-234-613-20
US-09-234-613-24
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PCT-US95-11808-4
US-08-337-8964-4
US-08-337-8964-4
US-08-337-401A-4
US-08-337-401A-4
US-08-337-401A-4
US-08-337-401A-4
US-08-337-2521A-4
US-08-337-2521A-4
US-08-337-2521A-4
US-08-337-2521A-4
US-08-337-2521A-4
US-08-337-2521A-4
US-08-337-2521A-4
US-08-337-2521A-4
US-08-726-214-4
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Sequence 27, Appl
Sequence 6, Appli
Sequence 16, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 30, Appli
Sequence 30, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 4, Appli
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US-08-796-899-27 Sequence 27, Application US/08796899 Patent No. 6160202 GENERAL INFORMATION: APPLICANT: BUSTOS, MAUTICIO MAPPLICANT: BUSTOS, MAUTICIO MATTLE OF INVENTION: TRANSCRIPTION FACTORS NUMBER OF SEQUENCES: 32 CORRESSER: BUTGS, DOAGNE, SWECKER & MATHIS STREET: P.O. BOX 1404 CITY: Alexandria STATE: Virginia COUNTRY: United States ZIP: 22313-1404 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY disk COMPUTER READABLE FORM: MEDIUM TYPE: PLOPPY disk COMPUTER READABLE FORM: MEDIUM TYPE: PLOPPY disk COMPUTER READABLE FORM: COMPUTER READABLE FORM: MAPPLICATION DATA: APPLICATION NUMBER: US/08/796,899 FILING DATE: 05-78B-1997 CLASSIFICATION DATA: APPLICATION NUMBER: US/08/796,899 FILING DATE: 07-OCT-1994 ATTORNEY/AGENT INFORMATION: NAME: MEUTH, DONGA M REGISTRATION NUMBER: US/08/796,899 FILING DATE: 07-OCT-1994 ATTORNEY/AGENT INFORMATION: NAME: MEUTH, DONGA M REGISTRATION NUMBER: US/08/796,899 FILING DATE: 07-OCT-1994 ATTORNEY/AGENT INFORMATION: TELECOMMUNICATION INFORMATION: TELEFAX: (703) 836-6620 TELEFAX: (703) 836-6620 TELEFAX: (703) 836-6620 TELEFAX: (703) 836-620 INFORMATION FOR SED ID NO: 27: SEQUENCE CHARACTERISTICS: LEGGIST STANDEDNESS: single TOPOLOGY: Linear MOLECULE TYPE: DNA (genomic)	28 39.5 28.0 358 1 US-08-239-431A-4 29 39.5 28.0 358 2 US-08-463-981B-6 30 39.5 28.0 358 2 US-08-461-379A-6 31 39.5 28.0 358 3 US-08-463-99A-6 32 39.5 28.0 358 3 US-08-463-974B-6 33 39.5 28.0 358 3 US-08-465-585C-6 34 39.5 28.0 358 3 US-09-083-351-2 35 39.5 28.0 553 4 US-09-083-351-2 36 39.5 28.0 553 4 US-09-083-352-2 37 39 27.7 346 3 US-09-083-352-2 39 39 27.7 346 4 US-09-387-922-2 40 39 27.7 447 4 US-09-378-255-2 41 39 27.7 475 4 US-09-378-255-2 42 39 27.7 574 4 US-09-251-372-2 43 39 27.7 880 2 US-08-484-438-6 44 39 27.7 880 3 US-09-251-70-12 45 39 27.7 880 4 US-09-225-170-12 45 39 27.7 880 4 US-09-141-212-4
	Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli

Query Match
Best Local Similarity
Matches 11; Conserv

Conservative

36.2%;

Score 51; DB pred. No. 3.2; Mismatches

DB 3.2; 4;

Length 552;

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REFERENCE/DOCKET NUMBER: 30, 727
REFERENCE/DOCKET NUMBER: 20747/30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1600
TELEPAX: (716) 263-1487
TELEX: 978450 (WUT)
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino
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Best Local Similarity
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Patent No. 5643779
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                                                                                                              APPLICANT: BARRY III, Clifton E.
APPLICANT: YUAN, YING
TITLE OF INVENTION: CLONING AND EXPRESSION OF DNA INVOLVED
TITLE OF INVENTION: IN THE BIOSYNTHESIS OF CYCLOPROPANATED MYCOLIC ACIDS
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: pr
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Godon, Jean-Jacques
APPLICANT: Renault, Pierre
TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
TITLE OF INVENTION: synthase from Lactococcus and its applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                       ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco
                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Lactococcus lactis subsp. lactis INDIVIDUAL ISOLATE: ILVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 570 amino acids
TYPE: amino acid
TOPOLOGY: linear
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94105-1493
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Pred. No.
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Matches 12; Conserv
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TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
               APPLICATION NUMBER: JP 221193/1997
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
                                                                                  FILING DATE: 26-SEP-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CELLOBIOSE PHOSPHORYLASE GENE, VECTOR TITLE OF INVENTION: AND TRANSFORMANT CONTAINING SAID GENE NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Guy W.
REGISTRATION NUMBER: 30,617
REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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187 LHTIIVPDAKETKELGLTTPMSL 209
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                                                                                                                                             APPLICATION NUMBER: US/08/939,002A
                                                                                                                                                                                                                                                                                                                  STATE:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                              ZIP: 22202
                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                 CITY: ARLINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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KITAMURA, YOSHIAKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAYASHI, KIYOSHI
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                                                                                                                          26-SEP-1997
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52.2%; Pred. No.
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                                                                                                                                                                                  Version
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US-09-074-044A-20; Sequence 20, Application US/09074044A; Patent No. 6207458
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; Sequence 20, Appli
; Patent No. 6160095
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Best Local Similarity
Whiches 6; Conserve
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SEQ ID NO 20
LENGTH: 139
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
FILE REFERENCE: Chaudhary
CURRENT APPLICATION NUMBER: US/09/382,155B
CURRENT FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: 09/074,044
EARLIER APPLICATION NUMBER: 09/074,044
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                     APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING
TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 822 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 373 LLGFVHLIPERARERIIDIAS 393
                                                                                 ALUDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS STREET: 2405 GRAND BLVD., SUITE 400 CITY: KANSAS CITY
                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                         73 LHLDPRFLERHLAGTMS 89
                                                                                                                                                                                                                                                                                                                                                                                                  8 LHIVPEFIESQLLGLLS 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                       64108
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                                                                      MISSOURI
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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OF USING THE SAME
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RESULT 7
US-08-818-514-3
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US-08-818-514-3
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                TELEPHONE: (619) 535-89 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 816/474-9057 INFORMATION FOR SEQ ID NO:
                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/074,044A
                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Reed, Joh APPLICANT: Xu, Qunli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73
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REGISTRATION NUMBER: 26
REFERENCE/DOCKET NUMBER:
                          LENGTH: 237 amino TYPE: amino acid
                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: UZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 4370 La
CITY: San Diego
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TOPOLOGY: nc
                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 816/474-9050
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 amino acids
                                                237 amino acids
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SYSTEM: PC-DOS/MS-DOS
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47.1%;
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16
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Pred. No. 9;
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CORRESPONDENCE ADDRESS:

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RESULT 8
US-09-115-934A-3
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                                                                                           Sequence 2, Application US/08403634 Patent No. 5674748 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  Query Match 31.2%;
Best Local Similarity 40.9%;
Matches 9; Conservative
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Best Local Similarity 40.9%;
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APPLICATION NUMBER: US 08/818,514
FILING DATE: 14 MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 3209
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 43/
STREET: A3/
CITY: San Diego
STATE: California
STATE: United States
APPLICANT: Giordano, Antonio
TITLE OF INVENTION: NOVEL HUMAN CYCLIN-DEPENDENT
TITLE OF INVENTION: KINASE-LIKE PROTEINS AND METHODS
TITLE OF INVENTION: OF USING THE SAME
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Reed, John C.
APPLICANT: Xu, Qunl1
TITLE OF INVENTION: BAX Inhibitor Proteins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            46 YVHMVTHFIQAGLISALGSLIL 67
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (619) 535-9001
(619) 535-8949
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Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                       Length 237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                  Patent No. 5674748

GENERAL INFORMATION:
APPLICANT: Glordano, Antonio
TITLE OF INVENTION: NOVEL HUMAN CYCLIN-DEPENDENT
TITLE OF INVENTION: KINASE-LIKE PROTEINS AND METHODS
TITLE OF INVENTION: OF USING THE SAME
NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 31.3
Best Local Similarity 47.6
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,575
FILING DATE: 08-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1482
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (215) 668-3439
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                       COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                      ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & ADDRESSEE: No. 5674748ris STREET: One Liberty Place, 46th floor CITY: Philadelphia
                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & ADDRESSEE: No. 5674748ris
STREET: One Liberty Place, 46th floor
                APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 424
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ZIP: 19103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYLHIVPEFIESQLLGLLSPV 26
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GY: linear
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47.6%; Pred. No.
                                                        US/08/403,634
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27;
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US-08-913-441B-30
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US-08-913-441B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08913441B Patent No. 6162612 GENERAL INFORMATION:
                                                                                                                                                                       Sequence 30, Application US/08913441B Patent No. 6162612
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
SEQ ID NO 2
                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/08/913,441B CURRENT FILING DATE: 1997-12-02 PRIOR APPLICATION NUMBER: 08/403,634 PRIOR FILING DATE: 1995-03-14 PRIOR APPLICATION NUMBER: PCT/US96/03557 PRIOR FILING DATE: 1996-03-14
            FILE REFERENCE: 8321-76 CI1
CURRENT APPLICATION NUMBER: US/08/913,441B
CURRENT FILING DATE: 1997-12-02
PRIOR APPLICATION NUMBER: 08/403,634
                                                      APPLICANT: Glordano, Antonio
TITLE OF INVENTION: No. 6162612el Human Cyclin-Dependent Kinase-Like Proteins and
TITLE OF INVENTION: Methods of Using The Same
FILE REFERENCE: 8321-76 CI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Giordano, Antonio
TITLE OF INVENTION: Mo. 6162612el Human Cyclin-Dependent Kinase-Like Proteins and
TITLE OF INVENTION: Methods of Using The Same
FILE REFERENCE: 8321-76 CI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: TJTTELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/208,575 FILING DATE: 08-MAR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                           97 GSIYLVFDFCEHDLAGLLSNV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 GSIYLVFDFCEHDLAGLLSNV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 31.2%;
Local Similarity 47.6%;
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: DEDUCE, REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                             6 GYLHIVPEFIESQLLGLLSPV 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 GYLHIVPEFIESQLLGLLSPV 26
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                                                                                                                                                                                                                                                                                                                                                                     10;
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                                                                                                                                                                                                                                                                                                                                                                     Conservative
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1995-03-14
                                                                                                                                                                                                                                                                                                                                                                                      31.2%;
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                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 4;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: Phosphorylation deficient PITALRE US-08-913-441B-30
; MOLECULE TYPE: US-09-036-987A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-036-987A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT. PRIOR FILING DATE: 1996-03-14 NUMBER OF SEQ ID NOS: 31
                                                                                                      TELEFAX: (317)337-484 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 372
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2595 amino acids
                                                                                                                                        TELEPHONE: (317)337-4816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                 TOPOLOGY:
                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 09-MAR-1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 9330 Zions CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 GSIYLVFDFCEHDLAGLLSNV 117
                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                      TELEPHONE:
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                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9330 Zionsville Road
                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                         (317)337-4847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Broughton, Mary C.
Crawford, Kathryn P.
Madduri, Krishnamurthy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Merlo, Donald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baltz, Richard H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dow AgroSciences LLC Patent Department
                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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47.6%;
                                                                                                                                                                                                                                                                                    US/09/036,987A
                                                                                                                                                                                              28,479
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                                                                                                                                                                               50,608
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Query Match
Best Local Similarity

31.2%;

Score 44; DB 4; Pred. No. 2.4e+02;

Length 2595;

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RESULT 14
5171684-7
5171684
PATENT NO. 5171684
PATENT NO. 5171684
PAPLICANT: YEN, KWANG-MU; BLATT, LAWRENCE M.; KARL, MICHAEL R.
HOLLOWITTE OF INVENTION: BIOCONVERSIONS CATALYZED BY THE TOULUENE
MONOXYGENASE OF PSEUDOMANAS MENDOCINA KR-1
UMUMBER OF SEQUENCES: 41
CURRENT APPLICATION NOMBER: US/07/590,374
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION UMBER: 177,631
FILING DATE: 05-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-08-933-750C-20
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
EILING DATE:
EILING DATE:
EILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 95,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 30.5%;
Best Local Similarity 58.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                        STREET: 3174 PORT
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GYLH-IVPEFIESQLLG 21
||:||:||:|| |||
275 GYVHEIIPEYMEG-LLG 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0, Application US/08933750C 5932442
                                                                                                                                                                                                                                                                                                                                                                                   3E: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shah, Purvi
Au-Young, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillman, Jennifer L.
Bandman, Olga
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Pred. No. 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
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Search completed: August
Job time: 294 sec
                                                                                                                                                                                                US-08-933-750C-20
                                                                                                                                                                                                                                                           TELEX:
INFORMATION FOR SEO ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                            TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUTO3
CLONE: 864683
                                                                   340 CIVGHQHMIPE 350
                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                             3 CVLGYLHIVPE 13
                                                                                                                         30.5%;
ilarity 45.5%;
Conservative
             7,
             2001, 13:29:00
                                                                                                                                                                                                                                                                                                                           20:
                                                                                                                          5; Mismatches
                                                                                                                                       Score 43; DB 2; Pred. No. 59;
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Gaps

0

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
SPTREMBL_16:*

1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:
12: sp_unclass:
13: sp_vertebr:
14: sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-251-133-6
141
1 RTCVLGYLHIVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    August 7, 2001, 13:28:41; Search time 23.02 Seconds (without alignments) 160.927 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                         425026 seqs, 132305027 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                            sp_archea:*
sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTCVLGYLHIVPEFIESQLLGLLSPVSL 28
                                                                            sp_organelle:*
sp_phage:*
                                                                                                              sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_unclassified:*
sp_vertebrate:*
sp_virus:*
                                                  sp_rodent:*
                                                               sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                              425026
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	% Query Match Length	DB	ID	Description
1	52	36.9	239		Q9MS96	Q9ms96 galdieria
N	52	36.9	889	ۍ	Q9VXB7	
ω	50	35.5	812	N	052504	-
4	50	35.5	813	N	087964	· .
رب ر	50	35.5	813	ν	Q9X2G3	_
6	49	34.8	275	N	206111	
7	48.5	34.4	469	տ	Q9VFE9	Q9vfe9 drosophila
80	48	34.0	99	σ	Q95309	Q95309 sus scrofa
9	48	34.0	512	U	Q9VZU3	
10	48	34.0	626	S	Q9U3X4	
11	48	34.0	702	ட	Q9YFQ8	Q9yfq8 aeropyrum
12	47	33. 3	146	10	Q9LRT3	Q9lrt3 arabidopsis
13	47	33.3	308	N	Q49807	Q49807 mycobacteri
14	47	33.3	496	w	Q04919	Q04919 saccharomyc
15	47	33. 3	532	_	027545	027545 methanobact
16	46.5	33.0	415	σ	018856	018856 caenolestes
17	46.5	33.0	550	10	Q9LLM4	Q91lm4 eucalyptus
18	46.5	33.0	554	IJ	Q93174	Q93174 caenorhabdi
19	46.5	ິດ	20	J	207141	

45	44	43	42	41	40	39	38	37	36	35	3 4	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20
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						31.9																			33.0
1319	1013	822	811	558	480	477	432	428	409	405	388	310	288	2048	871	643	425	425	395	4684	964	662	179	169	913
10	14	N	Ν	w	N	N											σ	δ	σ	4	11	10	N	10	S
Q9SLE9	Q9Q078	066264	Q59316	P87161	Q9F8X3	Q9KKT5	004473	Q9EYG4	P91783	Q9U3D1	067472	Q98240	P96312	Q9SIF1 ·	Q9YCK9	Q9LR59	018860	018859	018857	Q15149	Q9QXS1	Q9M9T8	083125	Q9SZV1	097272
Q9sle9 arabidopsis	Q9q078 chimpanzee	066264 cellvibrio	Q59316 clostridium	P87161 aspergillus	Q9f8x3 pseudomonas	Q9kkt5 vibrio chol	004473 arabidopsis	Q9eyg4 vibrio chol	P91783 polyorchis	Q9u3d1 caenorhabdi	067472 aquifex aeo	Q98240 molluscum c	P96312 burkholderi	Q9sifl arabidopsis	Q9yck9 aeropyrum p	Q91r59 arabidopsis	O18860 vombatus ur	018859 dromiciops	018857 phascogale	Q15149 homo sapien	Q9qxs1 mus musculu	Q9m9t8 arabidopsis	OB3125 treponema p	Q9szvl arabidopsis	097272 plasmodium

ALIGNMENTS

RESULT Q9VXB7 ID Q AC Q	Db Qy	Que Bes Mat	SQ	DR R	DR	DR DR	DR	DR	R R	RC	R 7	×	8	റ്റ	8	So	DΕ	DT	Ŋ	ΡŢ	AC	ID Q	RESULT
17 2 37 09VXB7 Q9VXB7;	1 RTCVLGY : 14 RKCILDN	Query Match Best Local Simi Matches 11;	Hypothetical SEQUENCE 2	SMART; SM00382; AAA; 1.	Pfam; PF00005;	InterPro; IF InterPro; IF	InterPro; IF	EMBL; AF2330	Whitney S.M., Andrews Submitted (FEB-2000)	STRAIN-UTEX 2393;	SEQUENCE FROM N.A	NCBI_TaxID=130081;		Eukaryota; F	Chloroplast.	Galdieria sulphuraria	HYPOTHETICAL	01-MAR-2001	01-OCT-2000	01-OCT-2000	Q9MS96;	Q9MS96	1
PRELIMINARY;	RTCVLGYLHIVPEFIESQLLGLLSP : : : :: KCILDNLHMTFSQYEILGLLGP	36.9%; Similarity 44.0%; 1; Conservative	Hypothetical protein; Chloroplast SEQUENCE 239 AA; 26836 MW; 58	SMART; SM00382; AAA; 1.)5; ABC_tran;	IPR003439;	IPR001687;	168	EB-2000) to the	2393;	M N.A.	.30081;		thodophyta;		ılphuraria.	26.8 KDA PR			(TrEMBLrel, 1		PRELIMINARY;	
PRT; 6	GLLSP 25 GLLGP 36	Score 52; Pred. No. 5; Mismat	oroplast. MW; 58A2868						he EMBL/GenBank/DDBJ					Bangiophyceae;				Last		15, Created)		PRT; 2	,
688 AA.		DB 8; Length 239; 7.1; ches 7; Indels	st. 58A2868B544A85FD CRC64;	CNONCHALL.	NOUN 1				nk/DDBJ databases.					Porphyridiales; Por					nce update)			239 AA.	
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RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Fosler C., Gabriellan A.E., Garg N.S., Gebart W.M., Glasser K.,

RA Harris N.L., Harvey D., Helman T.J., Welman P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Welman P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Welman B., Harris M., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Keinert K., Mary M., Welson D.L.,

RA Keinert K., Mary M., Welson D.L.,

RA Wang X., Welson K.A., Nixon K., Nusskern D.R., Sunen H.,

RA 
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Best Local
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052504;
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CG4724 PROTEIN.
CG4724.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Etukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pfam; PF01603;
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                                                                                                                                                                                       CVLGYLHIVPEFIESQLLGLL
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Last annotation update)
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Pred.
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087964;
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01-NOV-1998
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Sequen
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PROSITE; PS00639; THIOLPROTEASE_HIS; UNKNOWN_1.
Transferase; Glycosyltransferase.
SEQUENCE 813 AA; 93677 MW; 04D4FF39E61AEA88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Z2706-MC24;
Zverlov V., Bronnenmeler
Zubmitted (OCT-1997) to 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and expression in Escherichia coli of Thermotoga neapolitana genes coding for enzymes of carbohydrate substrate degradation."; Biochem. Biophys. Res. Commun. 194:1359-1364(1993).

EMBL; Z99777; CAB16926.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93356813; PubMed-8352795;
Dakhova O., Kurepina N., Zverlov V.,
Velikodvorskaya G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermotoga neapolitana. Bacteria; Thermotogales;
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ILGFVHMIPEKARQRILDLAS 387
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8; Conserv
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8; Conser
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 13, Last annotation update)
PHOSPHORYLASE (EC 2.4.1.20).
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MEDLINE-99287316; PubMed-10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

Haft D.H., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heldelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria fro
                                                                                                                                                                                                                                                                                                                                                 Q06111;
Q06111;
                                                                                                                                Holck A.L., Blom H.;
"The nucleotide sequence of a putative Clostridium perfringens.";
DNA Seq. 3:191-194(1992).
-I- FUNCTION: MAY BE PART OF A BINDING-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
PROSITE; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9X2G3;
01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                      Clostridium perfringens.
Bacteria; Firmicutes; Ba
                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TREMBLIEL 01, 01-NOV-1996 (TREMBLIEL 01, 01-MAY-2000 (TREMBLIEL 13,
                                                                                                                                                                                             STRAIN-NCTC 8239;
MEDLINE-93113001;
                                                                                                                                                                                                                                                                                                PUTATIVE TRANSPORT SYSTEM PERMEASE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001822; AAD36910.1; -. TIGR; TM1848; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermotoga maritima
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               NCBI_TaxID=1502;
                                                                                                                                                                                                                                                             Clostridium
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                                     Pfam;
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                                             PROTEIN-DEPENDENT TRANSPORT
L; X66092; CAA46887.1; -.
erPro; IPR000515; -.
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SIMILARITY: WITH INTEGRAL MEMBRANE
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                                                                                                          SUBCELLULAR LOCATION:
                                                                                                                         SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                         ILGFVHMIPEKARQRILDLAS
membrane; Tr
VCE 275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; IPR000169; -.
PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
813 AA; 93499 MW; 55FC07E7329D8C41 CRC64;
                       00528; BPD_transp; 1.
PS00402; BPD_TRANSP_INN_MEMBR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermotogales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM N.A.
/ DSM 3109;
                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
Transport;
                                                                                                                                                                                                PubMed-1472712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.5%;
                                                                                                                                                                                                                                                                        Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,<u>;;</u>;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermotoga.
MW.
                                                                                                            INTEGRAL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                         387
           Transmembrane
                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                    BINDING-PROTEIN-DEPENDENT TRANSPORT
CC6B951258772772 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No ;
                                                                                                                                                                                                                                                                                                                                                             275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
52;
                                                                                   COMPONENTS OF
                                                                                                                                                                       membrane transport gene
                                                                                                                                                                                                                                                                                                                                                             ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                            PROTEIN.
                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                          INNER MEMBRANE
                                                                                   OTHER BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT
Q9VFE9
Qy
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                                       Addams D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Mannatides P.G., Scherer S.E., Li PW., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.R.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.R.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.R.,
RA Gentis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Durbin K.J., Evangelista C.C., Ferriera S., Fleischmann W.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Hehman T.J., Herrandez J.R., Houck J.,
RA Harris N.L., Harvey D., Hehman T.J., Herrandez J.R., Houck J.,
RA Liu X., Mattei B., McIntosh T.C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Palazzolo M., Hushon K., Sunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylraks R., Tector C. Turner R., Venter E., Wang A.H., Wang X.,
RA Globs R.A., Mysts E.W., Wolser S., Zhou X., Smith H.O.,
RA Globs R.A., Mysts E.W., Shon M., Shon S., Zhou X., Smith H.O.,
RA Globs R.A., Mysts E.W., Shon M., Shon S., Zhou X., Smith H.O.,
RA Globs R., Person B., Sun E.,
RA Globs R., Perso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000
01-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9VFE9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9VFE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 IFIVPQFLLVQKLGLLNTIS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 LHIVPEFIESQLLGLLSPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN.
                                IPR002728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.) (TrEMBLrel.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
 Diphthamide_syn; AA; 52095 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.8%;
50.0%;
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14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          core 49; DB ced. No. 23; Mismatches
 4D149090874896A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hexapoda; Insecta;
a; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                       H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                     K.A.,
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RESULT
Q9VZUJ
AC Q9VZUJ
AC Q9VZUJ
DT DT Q9
DT Q9
OC GRO
OC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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Best Local S
Matches S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09VZU3;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
CG15812 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q95309;
Q95309;
Q1-FEB-1997
                  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S. A., Danburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtls K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Gebalos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CG15812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9VZU3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-SMALL INTESTINE;
Winteroe A.K., Fredholm M.,
Submitted (JUL-1995) to the
EMBL; Z81159; CAB03546.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1997
01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|:| ||:: || | : |
46 YVHVVTRFIQAGLLSALGSLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RTCV----LGYLHIVPEFIESQLLGLLSPVSL 28
: || :|| |: | :: || :| | |
56 QVCVYLDIGYQHYYGEKLKKQLSEILEPKEL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 YLHIVPEFIESQLLGLLSPVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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     Doup L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 AA; 10846 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.0%;
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     Downes
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13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Davies W.;
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
     33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48.5;
Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EA009C94B5EE6211 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Dugan-Rocha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  512 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
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  Dew I., Dietz S.M.,
S., Dunkov B.C., Dun
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     PRINTS; PR00368;
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RA Durbin K.J., Evangelista C.C., Ferriaz C., Ferriara S., Fleischmann W., Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.A., Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Ra Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C., Ra Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Ra Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Ra Lasko P., Lei Y., Levitaky A.A., Li J., Li Z., Liang Y., Lin X., Ra Lasko P., Lei Y., Levitaky A.A., Li J., Li Z., Liang Y., Lin X., Ra Lasko P., Lei Y., Levitaky A.A., Li J., J. Z., McPherson D., McShot S.M., Wolson K.A., Nixon K., McLeod M.P., McPherson D.L., Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Nount S.M., Welson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Menson D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Ra Syler E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Ra Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Zheng X.H., Zhong E.W., Rubin G.M., Venter J.C., Rhou X., Smith H.O., Ra Zheng X.H., Zhong E.W., Rubin G.M., Venter J.C., Rhu X., Smith H.O., Rh Glbbs R.A., Nyers E.W., Rubin G.M., Venter J.C., Rhu X., Smith H.O., Rh Glbbs R.A., Nyers E.W., Rubin G.M., Venter J.C., Rhu X., Smith H.O., Rh Glbbs R.A., Nyers E.W., Rubin G.M., Venter J.C., Rhu X., Smith H.O., Rh Glbbs R.A., Nyers E.W., Rubin G.M., Venter J.C., Rhu X., Smith H.O., Rhu Y., Shi Rhu Y
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Best Local S
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InterPro: IPR0002672; ...
Pfam; Pf00651; BTB; 1.
ProDom; Pp010767; .; 1.
PROSITE; PS50097; BTB; 1.
SMART; SM00225; BTB; 1.
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Q9U3X4;
01-MAY-2000
01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                        STRAIN-AX2;
Lay S.P., Fi
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EMBL; AE003477; AAF47724.1; -.
FlyBase; FBgn0035405; CG15812.
                                                                                                                 EMBL; AF211482; AAF21045.1; HSSP; P00363; 1FUM.
                                                                                                                                                                                               -!- COFACTOR: FAD (BY SIMILA -!- SIMILARITY: TO PYRIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                                              Submitted (DEC-1999) to the
                                                                                                                                                                                                                                                                                      dehydrogenase.";
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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  Pfam;
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  PF00890;
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11; Conservative
                       IPR001100;
IPR001327;
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                                                                                   IPR000464; -.
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FAD_binding_2; 1.
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Best Local S
Matches 9
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A Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosug
A Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
A Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
A Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
T'Complete genome sequence of an aerobic hyper-thermophilic
Trenarchaeon, Aeropyrum pernix K1.";
DNA Res. 6:83-101(1999).
C -!- SIMILARITY: TO DEAD/DEAH BOX HELICASE FAMILY.
R EMBL; AP000058; BAA79103.1; -.
R InterPro, IPR000445; -.
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Matches
OSLRT3;
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O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
O1-OCT-2000 (TREMBLREL. 15, Last annotation update)
GENOMIC DNA, CHROMOSOME 3, P1 CLONE:MMGI5.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Embryophyta; Tracheophyte
Bukaryota; Viridiplantae; Embryophyta; Tracheophyte
Magnoliophyta; eudicotyledons; core eudicots; Rosi(
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PROSITE; PS00504; FI
FAD; Flavoprotein; (
SEQUENCE 626 AA;
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Pfam; PF00271; helicase_C;
SMART; SM00490; HELICC; 1.
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01-NOV-1999 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
702AA LONG HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding; Helicase.
SEQUENCE 702 AA; 76717 MW;
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                                                                                                                                                                                                                                           Q9LRT3
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; FRD_SDH_FAD_BINDING; 1.
; VOXIdoreductase; Redox-active
a; 68515 MW; C8F27868BD063D67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed-10382966;
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HELICASE.
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Pred. No.
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Pred. No.
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                                                                     Tracheophyta;
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Sequence features of the region:
TAC and BAC clones.";
DNA Res. 7:217-221(2000).
EMBL; AB028616; BAB01124.1; -.
SEQUENCE 146 AA; 16686 MW;
                                                                                   Submitted (MAR-1994) to the EMBL; U00018; AAA17222.1; Interpro; IPR001051; Interpro; IPR001501; Interpro; IPR001333; Pfam; PF02353; CMAS; 1.
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Submitted (JUN-1999)
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O1-MAR-2001 (TrEMBLrel. 16, La
PHENYLALANYL-TRNA SYNTHETASE A
                                                            Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
EMBL; AE000910; AAB85976.1; -.
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Saccharomyces cerevisiae (Baker's yeast).
Elikaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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InterPro;
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EMBL; Z48612; CAA88496.1; -
SGD; S0002624; ADRI.
SGD; S0002624; ADRI.
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STRAIN-DELTA H;
MEDLINE-98037514; PubMed-9371463;
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rhipicephal
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                                                                                     human
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                                                                                                                                                                                                                           marinu
                                                                                   herpe
                                                                                                                                                                                                                 gall
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Walter L.,

Dirks B.,

Rothermel E., Heyens M.,

Szpirer C., Levan G.,

Juenther E.;

'A novel, conserved gene of the rat that is developmentally regulated

STRAIN-SPRAGUE-DAWLEY; TISSUE-Testis; MEDLINE-94281747; PubMed-8012111;

NCBI_TaxID=10116;

SEQUENCE FROM N.A.

BI1 OR TEGT.

ALIGNMENTS

RESULT BI1_RA RAT

BII_RAT STANDARD: PRT; 236 AA. P55062; Q64712; Q1-QCT-1996 (Rel. 34, Created) Q1-QCT-1996 (Rel. 34, Last sequence update) Q1-QCT-2000 (Rel. 40, Last annotation update) BAX INHIBITOR-1 (BI-1) (TESTIS ENHANCED GENE TRANSCRIPT).

Rattus norvegicus (Rat). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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Query Match
Best Local Similarity
""" Phes 9; Conserve
                                                                    TRANSMEM
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SEQUENCE
                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                         in the testis.";

Mamm. Genome 5:216-221(1994).

-i- FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).

-i- SUBGURIT: INTERACTS WITH BLC2 AND BCL-YL (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

-i- TISSUE SPECIFICITY: HIGHLY ABUNDANT IN TESTIS.

-i- SIMILARITY: BELONGS TO THE BI1 FAMILY.
                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                    Apoptosis;
TRANSMEM
                                                                                                                                                                          Pfam; PF01027; UPF0005; 1. PROSITE; PS01243; BI1; 1.
                                                                                                                                                                                                            EMBL; X75855; CAA53470.1; EMBL; X75856; CAA53471.1;
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                                                                            Transmembrane.
30 50
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POTENTIAL.
                       Score 49; DB 1;
Pred. No. 2.4;
                                  Length 236;
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Conservative

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Mismatches

Indels

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Gaps

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67 28

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IFA2_MYCTU

ID CFA2_MYCTU

ID CFA2_MYCTU

ID CFA2_MYCTU

ID CFA2_MYCTU

ID CFA2_MYCTU

ID CQ11196;

AC Q11196;

DT 01-0CT-1996 (Rel. 34, Created)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 39, Last annotation update)

DE CYCLOPROPANE FATTY ACVL PHOSPHOLIPID SYNTHASE 2 (EC 2.1 DE (CYCLOPROPANE FATTY ACID SYNTHASE) (CFA SYNTHASE) (CYCL MYCOLIC ACID SYNTHASE 2).

GN CMA2 OR RV0503C OR MTCY20G9.30C.

MYCODACTETIUM tuberculosis.
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ID VILVD_L
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Best Local S
Matches 9
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'fam; PF00920; ILVD_EDD; 1.

PROSITE; P$00886; ILVD_EDD_2; 1.

PROSITE; P$00887; ILVD_EDD_2; 1.

Branched-chain amino acid biosynthesis; Lyase; Iron-sulfur.

Branched-chain amino acid 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-JUL-1993
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-I- CATALYTIC ACTIVITY: 2,3-DIHYDROXY-3-METHYLBUTANOATE OXOBUTANOATE + + (2)0.
-I- COFACTOR: BINDS A 2FE-2S CLUSTER (POTENTIAL).
-I- PATHWAY: FOURTH STEP IN VALINE AND ISOLEUCINE BIOSYN-1- SIMILARITY: BELONGS TO THE ILVD / EDD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1993
15-DEC-1998
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MEDLINE-93015710; PubMed-1400210;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U92974; AAB81918.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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9; Conservative
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(Rel. 37, Last annotation update)
CID DEHYDRATASE (EC 4.2.1.9) (DAD)
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ADRI_YEAST
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AC PO7248
AC PO7248
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GN ADRI C
OS Sacche
OC Eukary
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Best Local
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                                                         ADRI_YEAST STAND
P07248:
01-APR-1988 (Rel. 07
01-APR-1988 (Rel. 07
15-JUL-1999 (Rel. 38
REGULATORY PROTEIN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-9829987; PubMed-9634230; Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                   REGULATORY PROTEIN ADR1.
ADR1 OR YDR216W OR YD8142.16 OR YD8142B.08.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; Methyltransferase; Lipid synthesis.

DOMAIN
76
84
SSENTIAL FOR CATALYSIS (PROBABI
SEQUENCE 302 AA; 34660 MW; 63AAA95627F95755 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; Z77162; CAB00929.1; -.
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"The biosynthesis of cyclopropanated mycollc acids in
tuberculosis. Identification and functional analysis
J. Biol. Chem. 270:27292-27298(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TubercuList;
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96070840;
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                                                                                                                                                                                                                                                                                       11 VPEFIESQLLGLLSPVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: TRANSFERS A METHYLENE GROUP FROM STADENOSYL-L-METHIONINE
TO THE CIS DOUBLE BOND OF AN UNSATURABLE FATTY ACID CHAIN
RESULTING IN THE REPLACEMENT OF THE DOUBLE BOND WITH A METHYLENE
BRIDGE. MYCOLIC ACIDS, WHICH REPRESENT THE MAJOR CONSTITUENT OF
MYCOBACTERIAL CELL WALL COMPLEX, ACT AS SUBSTRATES.
CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + PHOSPHOLIPID
OLEFINIC FATTY ACID - S-ADENOSYL-L-HOMOCYSTEINE + PHOSPHOLIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYCLOPROPANE FATTY ACID.
SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                         STANDARD;
                                                                            07, Created)
07, Last sequence update)
38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                33.3%;
                                                                                                                                                                                                                                                        203
                                                                                                                                                                                                                                                                                                                                                Score 47;
Pred. No.
 Saccharomycotina;
                                                                                                                                                                                                                                                                                                                               Mismatches
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Eukaryota;

Ascomycota;

Saccharomycetes;

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Slr.
Oliver k.
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                                                                                                                                                                                                                                                      MEDLINE-92195295; PubMed-1549108; Denis C.L., Fontaine S.C., Chase D., Kemp B.E., B "ADR1c mutations enhance the ability of ADR1 to a transcription by a mechanism that is independent AMP-dependent protein kinase phosphorylation of SMO1. Cell. Biol. 12:1507-1514(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thukral S.K., Morrison M.L., Young E.T.;
"Alanine scanning site-directed mutagenesis of the zinc transcription factor ADR1: residues that contact DNA and transactivate.";
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"A folding transition and novel zinc
transcription factor ADR1.";
Nat. Struct. Biol. 6:478-485(1999).
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MEDLINE-93078777; PubMed-1448103; Camier S., Kacherovsky N., Young E.T.; "A mutation outside the two zinc fingers in either finger."; Mol. Cell. Biol. 12:5758-5767(1992).
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MEDLINE-99260744; PubMed-10331877;
Bowers P.M., Schaufler L.E., Klevi
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Nature 320:283-287(1986).
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R.X., Horvath S.J., Klevit R.E.;
DRla, a zinc finger peptide, exists
ochemistry 30:3365-3371(1991).
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"Mutations in the zinc-finger region of the ADR1 affect both DNA binding and transcripti J. Biol. Chem. 269:9374-9379(1994).

-I- FUNCTION: REQUIRED FOR TRANSCRIPTIONAL A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear protein; on; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rovelli A.,
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(Rel. 25, Created)

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RESULT
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Best Local s
Matches 9
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                                                                     IRF3_CHICK
Q90643;
Q1-NOV-1997
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Achen M.G., Harms P.J., Thomas T., Richardson S.J., Wettenhall R.E.H., Schreiber G., Protein synthesis at the blood-brain barrier. The major protein secreted by amphibian choroid plexus is a lipocalin."; J. Biol. Chem. 267:23170-23174(1992).
                           Gallus gallus (Chicken).
                                          01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
INTERFERON REGULATORY FACTOR 3 (IRF-3).
                                                                                                                                                                                                  CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00061; lipocalin; l. PRINTS; PR00179; LIPOCALIN. PRINTS; PR01254; PGNDSYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Choroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bufo marinus (Giant toad) (Cane
Eukaryota; Metazoa; Chordata; Cr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Last 01-NOV-1995 (Rel. 32, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipocalin;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002972; -
Pfam; PF00061; lipocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                              17
                                                                                                                                                                                                                                                                                                                                           3 CVLGYLHIVPEFIESQLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: SECRETED INTO THE CEREBROSPINAL FLUID. TISSUE SPECIFICITY: EXPRESSED MAINLY IN CHOROID PLEXUS. MUCH LOWER EXPRESSION IN OTHER BRAIN AREAS, AND ABSENT FROM LIVER. DEVELOPMENTAL STACE: EXPRESSED THROUGHOUT AMPHIBIAN METAMORPHOSIS. SIMILARITY: BELONGS TO THE LIPOCALIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: MIGHT HAVE A TRANSPORT FUNCTION ACROSS THE BLOOD BRAIN BARRIER. IS SUPPOSED TO HAVE SIMILAR FUNCTIONS AS TRANSTHYRETIN WHICH MUST HAVE EVOLVED AFTER THE STAGE OF THE AMPHIBIANS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: MONOMER.
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                                                                                                                                                                                                                                                                                              CVYGDVPIQPDFQEDKILG
                                                                                                                                                                                                                                                                                                                                                                                          Similarity 47.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00213; LIPOCALIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
83
183
  Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
                                                                        (Rel. 35, Created)
(Rel. 35, Last seq
(Rel. 35, Last ann
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                                                                                                                                                                       STANDARD;
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183
179
Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND SEQUENCE OF 1-16; 18-20;
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47
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Pred. No.
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                                                                                                                                                                       PRT;
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  Euteleostomi;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grant C.E., Vasa M.2., Deeley R.G.;

"CIRF-3, a new member of the interferon regulatory factor (IRF)
family that is rapidly and transiently induced by dsRNA.";

Nucleic Acids Res. 23:2137-2146(1995).

-I- FUNCTION: MAY ACTIVATE TRANSCRIPTION BY COMPLEX FORMATION WITH
OTHER TRANSCRIPTIONAL FACTORS, POSSIBLY MEMBERS OF THE STAT
FAMILY. BINDS SPECIFICALLY TO THE IFN-STIMULATED RESPONSE ELEMENT
(ISRE) BUT NOT TO THE IRF-1 BINDING SITE PRD-I.

-I- SUBCELLULAR LOCATION: NUCLEAR.

-I- SIMILARITY: BELONGS TO THE IRF FAMILY.
                                                                                             Wiche G., Becker B., Luber K., Weitzer G.,
Hauptmann R., Stratowa C., Stewart M.;
"Cloning and sequencing of rat plectin ind
chain with a three-domain structure based
                                                                                                                                                                                                                                                                                          PLEC1
                                                                                                                                                                                                                                                                                                                                                                                                          RAT
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Transcription regulation; DNA-binding; Nuclear protein;
Transcription regulation; TRYPTOPHAN PENTAD REPEAT.

TRYPTOPHAN PENTAD REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
TISSUE=Glial tumor;
MEDLINE=96210632; PubMed=8633055;
                                                                              coiled
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                           PLECTIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00605; IRF; 1.
PRINTS; PR00267; INTERNREGECT.
PROSITE; PS00601; IRF; 1.
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HSSP; P15314; 1IF1.
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Gallus.
                                                                                                                                                            MEDLINE-91268156;
                                                                                                                                                                              TISSUE=Glial tumor;
                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
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                                 REVISIONS
                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM
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                                                                               coil
                                                                Biol.
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                                                               114:83-99(1991).
                                                                                                                                                              PubMed-2050743;
                                                                                                                                                                                                                                                         Chordata;
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Pred. No.
                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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                                                                                              indicates a 466-kD polypeptide
sed on a central alpha-helical
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                                                                                                                                             Castanon M.J.,
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THE TENERAL TRANSPORTATION OF THE TENERAL DRANGER OF THE TRANSPORTATION OF THE TRANSPORT
    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of variants with distinct Genomics 42:115-125(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001101; -. InterPro; IPR001715; -. Pfam; PF00307; CH; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97321050;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Plectin transcript diversity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: A TETRAMERIC STRUCTURE IS PROPOSED WHERE THE TWO CHAINS IN ONE MOLECULE ARE PARALLEL TO ONE ANOTHER AND THE TWO MOLECULE. ARE ARRANGED ANTIPARALLEL AND OVERLAP TO A GREAT EXTENT. ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1 (SHOWN HERE), 2, 3 AND 4; ARIPRODUCED BY ALTERNATIVE SPLICING.

PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN SKELETAL MUSCLE AND LOWEST IN THYMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: TO DESMOPLAKIN AND TO BULLOUS CAUTION: ISOFORM 4 IS A FRAGMENT AT THE N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A39638; A39638.
S21876; S21876.
; Q01082; 1AA2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: PLECTIN IS PROPOSED INTERMEDIATE FILAMENTS, TO INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X59601; CAA42169.1; -. U96274; AAC53209.1; -. U96275; AAC53210.1; -. U96276; AAC53211.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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U.S.A. 93:4278-4283(1996).
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INTERACTION WITH VIMENTIN AND LAMIN B
6 X TANDEM REPEATS OF MOTIF A.
MOTIF A (APPROXIMATE).
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R2 COILED COIL.
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REPEAT
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                                                                                                                     STRAIN-LB555 / E
Stirewalt V.L.,
                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-91117189; Michalowski C.B.,
                                                                                                                                                                            "The
                                                                                                                                                                                                                                                 Cyanophora paradoxa
                                                                                                                                                                                                                                                                            01-FEB-1996
01-OCT-2000
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DOMAIN
     modified
                                                                                                              Bryant D.A.;
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             ween the Swiss Institute of Bioinformatics Institute, by non-profit institute.
                                                                                                                                                                                                                                                                                                                                                                            7 YLHIVPEFIESQLLGLLSPVSL
                                                          CYANELLE ENDOPLASMIC RETICULUM (CER) MEMBRANES. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMII
                                                                                              FUNCTION: INVOLVED
                                                                                    OTHER PROTEINS TO ALLOW THE TRANSLOCATION OF PROTEINS
                                                                                                                                                                          alowski C.B.,
cyanelle S10
                                                                                                                                                                                                                                                                                                                                                           YLHLPPEIVPASLQRVRRPVAM
                                        SWISS-PROT entry is copyright.
                                                                                                                                                          Gen. Genet. 224:222-231(1990)
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8; Conser
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)0 (Rel. 40, L
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52
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                                                          BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
                                                                                                                      Michalowski C.B., Luffelhardt W.,
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                             ry is copyright. It is produced through a collaboration - Institute of Bioinformatics and the EMBL outstation -
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Last annotation update)
E SECY SUBUNIT.
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MOTIF A (APPROXIMATE).
MOTIF A (APPROXIMATE).
MOTIF A (APPROXIMATE).
6 X 19 AA REPEATS.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RON_HUMAN
Q04912;
01-OCT-1994
                                                                                                                                                                Wang M.-H., Ronsin C., Gesnel M.-C., Cou
Leonard E.J., Breatnach R.;
"Identification of the ron gene product
macrophage stimulating protein.";
Science 266:117-119(1994).
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING MEDLINE=96413302; PubMed=8816464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (EC 2.7.1.112)
(MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN).
                                                                                                                                                                                                                                                                          Collesi C., Santoro M.M., Gaudino G., Comoglio P.M.;
"A splicing variant of the RON transcript induces constitutive tyrosine kinase activity and an invasive phenotype.";
Mol. Cell. Biol. 16:5518-5526(1996).
                                                                                                                                                                                                                                                                                                                                                              Oncogene 8:1195-1202(1993).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Keratinocytes;
MEDLINE=93241719; PubMed=8386824;
Ronsin C., Muscatelli F., Mattei M.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00303; SECYTRNICASE.
PROSITE; PS00755; SECY_1; 1.
PROSITE; PS00756; SECY_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                         family
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                      vEDLINE=95025877; PubMed=7939629;
                                                                                                                                                                                                                                                   FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                        "A novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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          TYROSINE-PROTEIN KINASE ACTIVITY.

CATALITIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSINE PHOSPHATE.

SUBUNIT: HETERODIMER FORMED OF AN ALPHA CHAIN AND A BETA
CHAIN WHICH ARE DISULFIDE LINKED.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; ISOFORM (SHOWN HERE)
ISOFORM DELTA-RON; ARE PRODUCED BY ALTERNATIVE SPLICING. DE
LACKS PART OF THE EXTRACELLULAR DOWAIN, OLIGOMERIZES AND IS
CONSTITUTIVELY ACTIVATED.
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                                                                                                                                                   FUNCTION: RECEPTOR FOR MACROPHAGE STIMULATING PROTEIN (MSP). HAS
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IPR002208; -.
SPECIFICITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            license agreement (See http://www.isb-sib.ch/announce/
license@isb-sib.ch).
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KERATINOCYTES, AND
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InterPro; IPR002999; -.
InterPro; IPR002999; -.
Pfam; PP01437; Plexin, repeat; 1.
Pfam; PF01433; Sema; 1.
Pfam; PF01833; TIG; 3.
Pfam; PF00069; PXTRKINASE; 1.
PRINTS; PR00109; TYRKINASE, ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
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PTM: PHOSPHORYLATED IN RESPONSE TO LIGAND BINDING (PR
SIMILARITY: BELONGS TO THE MET TYROSINE KINASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DATABASE: NAME-PROW; NOTE-CD guide CDw136 entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cdw136.htm".
QVCVDGECHILGRVVRPGPDGVPQSTLLGILLPLLL 967
                                                     RTCVLGYLHIVPEFI---
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IPR001245; -.
IPR001627; -.
IPR002165; -.
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MSP RECEPTOR ALPHA CHAIN (POTENTIAL).
MSP RECEPTOR BETA CHAIN (POTENTIAL).
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W; EE782D07E4D2568A CRC64;
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MACROPHAGE-STIMULATING
                                                                                                           Mismatches
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RESULT 10

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Best Local
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P55061; OI
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APOPTOSIS;
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                                                                                                                                                                                                                                                                                                                                                                                                     "Bax inhibitor-1, a mammalian apoptosis suppressor i functional screening in yeast.";
MO1. Biol. Cell 1:337-346(1998).
-!- FUNCTION: SUPPRESSOR OF APOPTOSIS.
-!- SUBUNIT: INTERACTS WITH BLC2 AND BCL-YL.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
-!- TISSUE SPECIFICITY: HIGHLY ABUNDANT IN TESTIS.
-!- SIMILARITY: BELONGS TO THE BI1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Walter L., Marynen P., Szpirer J., Le "Identification of a novel conserved Genomics 28:301-304(1995).
                                                                                                                                                                                                                                                                 EMBL; X75861; CAA53472.1; -. EMBL; AF033095; AAB87479.1; MIM; 600748; -.
                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Cowling R.T., Birnboim Submitted (NOV-1997) to
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01-OCT-1996 (Rel.
01-OCT-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xu Q., Reed J.C.; "Bax inhibitor-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96015061; PubMed=8530040;
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Mammalia; Eutheria; Primates;
                                                                                                     SEQUENCE
                                                                                                                CONFLICT
                                                                                                                                                                                                                                           Pfam; PF01027;
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YVHMVTHFIQAGLLSALGSLIL
                     YLHIVPEFIESQLLGLLSPVSL
                                            Similarity
9; Conserv
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llarity 40.9%;
Conservative
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Pred. No.
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Catarrhini; Hominidae;
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                                            Mismatches
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RESULT 11

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Best Local :
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          CDK9_HU
P50750;
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"Mitochondrial gene order is not conserved and metastriate tick mitochondrial genomes.
Mol. Blol. Evol. 15:1772-1785(1998).
-!- CATALYTIC ACTIVITY: NADH + UBIQUINONE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NU1M_RHISA STANDARD; PRT; 313 AA.
099824;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3).
SEQUENCE FROM N.A. MEDLINE-95209665;
                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                    CDK9
                                                                                                                                                                            KINASE PITALRE) (C-2K).
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01-OCT-1996 (Rel. 34,
01-OCT-2000 (Rel. 40,
CELL DIVISION PROTEIN
                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=99083443; PubMed=9866211;
                                                                                     SEQUENCE FROM N.A. MEDLINE=94224836;
                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=34632; [1]
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                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                               HUMAN
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                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                       Rel. 34, Last sequence update)
Rel. 40, Last annotation update)
PROTEIN KINASE 9 (EC 2.7.1.-) (
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                                                                                                                                                                                                                                               STANDARD;
 PubMed=7695608
                                                                                                                                 Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                            31.2%;
                                                                                                                                                                                                                        Created)
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Pred. No.
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                                                                                                                                 Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                               PRT;
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COMPLEX I SUBUNIT 1
                                                                                                                                                                                                                                                                                                                                                  Mismatches
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19;
                                                                                                                                             Vertebrata;
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                                                                                                                                  Hominidae;
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                                                                                                                                                                                         (SERINE/THREONINE-PROTEIN
                                                                          P.P.,
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                                                                                                                                                                                                                                                                                                                                                                       Length 313;
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                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                             Euteleostomi;
                                                                           Rosenblatt J.,
                                                     phosphorylates
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SUMT_YEAST
ID SUMT_Y
AC P36150
DT 01-JUN
DT 01-JUN
DT 01-NOV
DE PROBAB
DE III ME
SN MET1 C
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                                                                                                                                     RESULT
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Best Local
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                                            SUMT_YEAST
P36150;
01-JUN-1994
01-JUN-1994
01-NOV-1997
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BINDING
ACT_SITE
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA polymerase II transcription.",

J. Biol. Chem. 274:34527-34530(1999).

J. Biol. Chem. 274:34527-34530(1999).

FUNCTION: MEMBER OF THE CYCLIN-DEPENDENT KINASE PAIR (CDK9/CYCLIN-FUNCTION) ENABER OF THE CYCLIN-DEPENDENT OF ELANGATION FACTOR B (P-TEFB), WHICH IS PROPOSED TO FACILITATE THE TRANSITION FROM ABORTIVE TO PRODUCTION ELONGATION BY PHOSPHORYLATING THE CTD (CARBOXY-TERMINAL DOMAIN) OF THE LARGE SUBUNIT OF RNA POLYMERASE (CARBOXY-TERMINAL DOMAIN) OF THE LARGE SUBUNIT OF KINASE ACTIVITY TOWARD CTD OF RNAP II AND CAN SUBSTITUTE FOR P-TEFB IN VITRO. IN VITRO, PHOSPHORYLATES RETINOBLASTOMA AND MYELLN BASIC PROTEIN.

SUBUNIT: ASSOCIATES WITH CYCLIN T TO FORM P-TEFB. ALSO ASSOCIATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROBABLE UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) (UROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L25676; AAA35668.1;
EMBL; X80230; CAA56516.1;
HSSP; P24941; 1AQ1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20044695; PubMed=10574912;
Fu T.J., Peng J., Lee G., Price D.H., Flores O.;
"Cyclin K functions as a CDK9 regulatory subunit and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best J.L., Presky D.H., Sw
"Cloning of a full-length
protein kinase from human
                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein kinase from hum
Biochem. Biophys. Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase;
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InterPro; IPR002290;
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SIMILARITY: BELONGS TO THE SER/THR FAMILY OF CDC2/CDKX SUBFAMILY.
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SUBCELLULAR LOCATION: NUCLEAR.
                 METHYLASE)
OR MET20
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42777,
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es. Commun.
                                                                                                                                                                                                                                                              31.2%;
               (UROPORPHYRINOGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA sequence encoding a endothelial cells."; mmun. 208:562-568(1995).
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
G > A (IN REF. 2).
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Pred. No. 23;
4; Mismatches
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69E851CC6F7A0388 CRC64;
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. 23;
              III METHYLASE)
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PROSITE; PS00840; SUMT_2; 1.
Methionine biosynthesis; Porphy
Methyltransferase.
SEQUENCE 593 Ab.
                                                                                                                                                                                                                                                                                                               Matches
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Best Local
                                                                                                          15-JUL-1999
PTS SYSTEM, OPERMEASE IIA
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Q45298;
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                        _BRELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z28294; CAA82148.1;
PIR; S38145; S38145.
SGD; S0001777; MET1.
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                          Actinomycetales;
NCBI_TaxID=92707;
                                                      Bacteria; Firmicutes; Actinobacteria;
                                                                   Brevibacterium lactofermentum
                                                                                               COMPONENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97157513; PubMed-9003798;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000878; -.
InterPro; IPR003043; -.
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                                                                                                                                                                                                                                                                                     6 GYLHIVPEFIESQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
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mitted (MAR-1994) to the
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8; Conser
                                                                                            7 (Rel. 35, Created)
7 (Rel. 35, Last sequence update)
9 (Rel. 35, Last sequence update)
9 (Rel. 38, Last annotation update)
9 (GLUCOSE-SPECIFIC IIABC COMPONENT (
IABC COMPONENT) (PHOSPHOTRANSFERASE
(EC 2.7.1.69) (EII-GLC/EIII-GLC).
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                           STANDARD;
                                         Corynebacterineae
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the EMBL/GenBank/DDBJ databases
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                                                       Actinobacteridae
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SEQUENCE FROM N.A

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Best Local S
Matches 9
                         METX_YEAST STANDARD; PRT; 649 AA. 00453; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) PUTATIVE CYSTATHONINE GAMMA-SYNTHASE (EC 4.2 SUCCINYLHOMOSERINE (THIOL)-LYASE).
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MOD_RES
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DOMAIN 1
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HSSP; P08837; 2F3G.
InterPro; IPR001127; -.
InterPro; IPR001996; -.
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nes 9; Conserv
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CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR PROTEIN HISTIDINE + SUGAR PHOSPHATE.
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EIIA DOMAI
POTENTIAL.
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                                                          4.2.99.9)
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Search completed: August Job time: 361 sec

7,

2001, 13:35:07

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В
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                                                                              Query Match
Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                        InterPro; IPR000277; -.
Pfam; PF01053; Cys_Met_Meta_PP; 1
Hypothetical protein; Methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gentles S., Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
SUBMITTER ACTIVITY: O-SUCCINYL-L-HOMOSERINE + L-CYSTEINE
CYSTATHIONINE + SUCCINATE (CAN ALSO USE HYDROGEN SULFIDE
                                                                                                                                                                Pyridoxal phosphate.
BINDING 451 4
                                                                                                                                                                                                                                           EMBL; Z46660; CAA86656.1;
SGD; S0004547; YML082W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
STRAIN-S288C / AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
347 KTVIFGFPYADTLHVLQEFNETYFLG 372
                             1 RTCVLGY-----LHIVPEFIESQLLG
                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: SECOND STEP IN METHIONINE BIOSYNTHESIS.
SIMILARITY: STRONG, TO N.CRASSA MET-7 AND TO YEAST YJR130C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METHANETHIOL AS SUBSTRATES)
                                                                              Similarity
                                                                                                                                               649 AA;
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / AB972;
                                                                                                                                             451 F
74313 MW;
                                                                              30.9%;
                                                               6.
                                                                              Score 43.5;
Pred. No. 49;
                                                                                                                                               PYRIDOXAL PHOSPHATE (POTENTIAL); FA952FBA0500BF6E CRC64;
                              21
                                                               Mismatches
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e biosynthesis; Lyase;
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                                                                                             Length
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                                                             Gaps
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Title:
Perfect score:
                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                Database :
                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  August 7, 2001, 13:25:16; Search time 15.4 Seconds (without alignments) 138.499 Million cell updates/sec
                                                                                                                                                                                                                                                                                             219241 segs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                           RTCVLGYLHIVPEFIESQLLGLLSPVSL 28
                                                                                                                                                                                                                                                         219241
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	ر ت	4	ω	N	_	No.	Result	
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preprotein translo	Ö				hypothetical prote	Œ	hypothetical prote	protein F21B7.27 [\sim	plectin - rat	hypothetical prote	interferon regulat	lipocalin - giant	די		hypothetical prote	regulatory protein	hypothetical prote	phenylalaninetRN	hypothetical prote		probable helicase	dihydroxy-acid deh	probable phosphogl	probable membrane	TEGT protein - rat	7	hetical pro	Description		

RESULT 2
A72203
A72203
Cellobiose-phosphorylase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Sate: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: A72203
C;Accession: A72203
C;Accession: A72203

Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316
A;Accession: A72203
A;Status: preliminary

A;Molecule type: DNA A;Residues: 1-813 <ARN> A;Cross-references: GB:AE001822; GB:AE000512; NID:g4982429; PIDN:AAD36910.1; PID:g498 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M.

ALIGNMENTS

Qy 3 CVLGYLHIVPEFIESQLLGLLSPV 26 : :: : : : Db 246 CLNQFVQNFPSLIESELMGMFSPL 269	Query Match 37.6%; Score 53; DB 2; Length 931; Best Local Similarity 37.5%; Pred. No. 6.5; Matches 9; Conservative 7; Mismatches 8; Indels 0; Gaps 0;	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-931 <sto> A;Cross-references: GB:AE005172; NID:g11079505; PIDN:AAG29216.1; GSPDB:GN00141 C;Genetics: A;Map position: 1</sto>	A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719 A;Accession: H86387	Nature 408, 816-820, 2000 A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.	R.Theologis, A. Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.	RESULT 1 H86387 H96387 hypothetical protein AAG29216.1 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

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A; Experimental s
C; Genetics:
A; Gene: TM1848
                                                                                                        R;Holck, A.L.; Blom, H.

DNA Seq. 3, 191-194, 1992
A;Title: The nucleotide sequence of a putative A;Reference number: A56641; MUID:93113001
A;Accession: A56641
                                                                                                                                                                                                  probable membrane transport protein - Clostridium perfringens C;Species: Clostridium perfringens C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_chancC;Accession: A56641
A;Cross-references: GB:X66092; NID:g296355; PIDN:CAA46887.1; PID:g296356 A;Note: nucleotide sequence not given; conceptual translation not comple: C:Superfamily: maltose transport protein malG
                                                      A; Molecule type: DNA
A; Residues: 1-275 <HOL>
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C; Superfamily:
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A; Molecule type: mRNA
A;Residues: 2-236 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: A novel, conserved gene of the rat that is developmentally regulated in the tesa;Reference number: I57015; MUID:94281747
A;Accession: I57015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995
C;Accession: S42069; IS7015; I76675
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A; Residues: 1-236 < RES>
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A; Residues: 1-236 <GUE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Guenther, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEGT protein -
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9; Conser
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8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         34.8%;
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                  complete
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A;Cross-references: GB:AE005176; NID:g12724193; PIDN:AAK05321.1; GSPDB:GN00146 A;Experimental source: strain IL1403 C;Genetics: C;Genetics: A;Gene: ilvD
                                                                                                                                                                                                                                                                                    C;Accession: G86777
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; 1
Genome Res. in press, 2001
A;Title: The complete genome sequence of the lactic acid bacterium
A;Reference number: A86625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: ilvD
C;Superfamily: dihydroxy-acid dehydratase
C;Keywords: branched-chain amino acid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Godon, J.J.; Chopin, M.C.; Ehrlich, S.D.
J. Bacteriol. 174, 6580-6589, 1992
A;Title: Branched-chain amino acid biosynthesis
A;Reference number: S35132; MUID:93015710
A;Accession: S35137
A;Molecule type: DNA
A;Residues: 1-570 <GOD>
A;Cross-references: EMBL:M90761; NID:92565137; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable phosphogluconate dehydratase (EC 4.2.1.12) - Lactococcus lactis su C;Species: Lactococcus lactis subsp. lactis C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000 C;Accession: S35137
                                                                                                                                 C; Superfamily: dihydroxy-acid dehydratase C; Keywords: carbon-oxygen lyase; hydro-lyase
                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-570 <STO>
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C; Accressor, R; Smith, D.R.; Robison, A. Smith, D.R.; Robison, A. Submitted to the EMBL Data Library, submitted to the EMBL Data Library,
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hypothetical protein B2168_F3_130 - Mycobacterium leprae
c;Species: Mycobacterium leprae
c;Date: 19-Mar_1997 #sequence_revision 25-Apr-1997 #text_
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70746
A;Description: Mycobacteri
A;Reference number: S72586
A;Accession: S72886
A;Status: preliminary
A;Molecule type: DNA
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A;Residues: 1-702 <KAW>
A;Cross-references: DDBJ:AP000058; NID:g5103388;
A;Experimental source: strain K1
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A;Reference number: A72450; MUID:99310339
A;Accession: E72775
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A;Title: Deciphering the biology of Mycobacterium
A;Reference number: A70500; MUID:98295987
A;Accession: B70746
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A;Experimental source: strain |
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A; Residues: 1-302 <COL>
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    Aeropyrum pernix (strain K1)

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                                  Query Match
Best Local Similarity
Matches 10; Conserv
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A; Title: Genome sequence of A; Reference number: A85480; A; Accession: B86033
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C;Keywords: aminoacyl-tRNA synthetase; ligase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phenylalanine--tRNA ligase (EC 6.1.1:20) alpha chain - Methanobacterium the N;Alternate names: phenylalanyl-tRNA synthetase alpha chain C;Species: Methanobacterium thermoautotrophicum C;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec:1997 #sequence_revision 05-Dec:1997 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                    hypothetical protein Z5002 [imported] - Escherichia coli (strain O157:H7) C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
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A; Residues: 1-532 <MTH>
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A;Cross-references: EMBL:U00018; NID:g467037; PIDN:AAA17222.1; PID:g467038
                                       A; Molecule type: DNA
A; Residues: 1-656 <STO>
                                                                                                                                                                             iller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                               C; Accession: B86033
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A;Cross-references: GB:AE005174; NID:g12518318; A;Experimental source: strain O157:H7, substrain
                                                                                      A; Status: preliminary
                                                                                                                                                                                                                          R; Perna, N.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                 QTEVYAYHPLLKEWVEVATFGLYSPIAL
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12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                            Plunkett III, G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.3%;
nilarity 52.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.3%;
                                                                                                                                 enterohemorrhagic Escherichia
MUID:21074935; PMID:11206551
                                                                                                                                                                                                     Burland, V.; Mau, B.; Glasr, N.W.; Lim, A.; Dimalanta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ű
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
  substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                      306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
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PIDN:AAG58726.1;
n EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 532;
                                                                                                                                                                                                     Glasner, J.D.; Rose, anta, E.; Potamousis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanobacterium thermoautotro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN: AAB85976.1;
                       GSPDB:GN00145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                       D.J.; May K.; Apoda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                         DWGP
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fu

Thermotoga maritima hypothetical

protein TM0280

Conservative

۲,

Mismatches

9;

Indels

0;

Gaps

0

33.3%;

Score 47; Pred. No.

DВ 37;

Length 656

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hypothetical protein C02C6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T18858
R;Swinburne, J
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19032
A;Accession: T18858
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-554 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Oliver, K.; Harris, D.

R;Oliver, K.; Harris, D.

A;Molecule type: DNA

A;Residues: 1-973 <OLI>
A;Coss-references: EMBL:268195; NID:g1122341; PID:e213845; PID:g1122349; MIPS:YDR216w

A;Experimental source: strain AB972
                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Murphy, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
A;Reference number: S59423
A;Accession: S59423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulatory protein ADR1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YD8142B.08; protein YD9934.01; protein YDR216w
C;Species: Saccharomyces cerevisiae
C;Date: 20-Aug-1987 #sequence_revision 20-Aug-1987 #text_change 06-Feb-1998
C;Accession: A24534; S59423; S59739; S61583
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A; Gene: SGD: ADR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-1215, 'H', 1217-1323 <DON>
A; Cross-references: EMBL: U28414; NID: 9924929; PID: 9924931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, June 1995
A;Description: cAMP-dependent protein kinase inhibits expression of the yeast transcript
A;Reference number: S59738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:248612; NID:g728671; PID:g728672; MIPS:YDR216w A;Experimental source: strain AB972 R;Dombek, K.M.; Young, E.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 828-1323 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-1323 <HAR>
A; Cross-references: EMBL: X03763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Sequence homology of the yeast regulatory protein ADR1 with Xenopus transcript: A;Reference number: A24534; MUID:86175015
A;Accession: A24534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Hartshorne, T.A.; Blumberg, H.; Young, E.T. 
Nature 320, 283-287, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No.
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                                                                                                                                                                                 20-Jun-2000
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                                                  Best
                                                                     Query Match
                                                  Local Similarity
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-179 <COL>
A;Cross-references: GB:AE001193; GB:AE000520; NID:g3322343; PIDN:AAC65082.1; PID:g332 A;Experimental source: strain Nichols
                                                                                                                                                                                 R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis A;Reference number: A71250; MUID:98332770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
"---hes 7; Conserv
                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein TP0087 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-
C;Accession: H71367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F6G3.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: X
A;Introns: 13/2; 126/3; 386/2; 419/2; 469/3; 525/3
C;Superfamily: Caenorhabditis elegans hypothetical
                                                                                                                                                      A; Accession: H71367
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C; Superfamily: Arabidopsis thaliana hypothetical protein F25G13.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AL078464; GSPDB:GN00062; ATSP:F6G3.10
A;Experimental source: cultivar Columbia; BAC clone F6G3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-169 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Bevan, M.; Murphy, G.; Ridley, P.; Hudson, submitted to the Protein Sequence Database, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z79596; PIDN:CAB01856.2; GSPDB:GN00028; CESP:C02C6.2 A;Experimental source: clone C02C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
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                        Genetics:
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Best Local :
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nes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 HIVPQWLDFSVISLMMPFS 111
TP0087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 HIVPEFIESQLLGLLSPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RTCVL------GYLHIVP---EFIESQLLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                      sequence of Treponema pallidum, the syphilis spirochete 50; MUID:98332770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46.5;
Pred. No. 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , S.; Bancroft, I.; Mewes, H.W.; Mayer, May 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 169
                                                                                                                                                                                                                                                                                 O.; Sutton, G.G.; Dodson, hidambaram, M.; Utterback,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 554;
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Conservative

32.6%;

Score 46; Pred. No.

DB 2; 13;

Length 179;

Mismatches

8,

Indels

0

Gaps

0

Qy 7 YLHIVPEFIESQLLGLLSPVS 27
||| |: |||||||:
Db 12 YLHRTPAALSLLLLGLLSCVA 32

Search completed: August 7, 2001, 13:29:28
Job time: 252 sec

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Result
No.
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
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1: /SIDS8/gcgdata,
2: /SIDS8/gcgdata,
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                                                                                                                                                                                                                                  Match
                                                                                                                                                                                                                                                   Query
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5: /SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:*
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen
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                       AAB48241
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AAW38569
AAW385687
AAB24844
AAB24844
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L.lactis branched
S. pneumoniae prot
Streptococcus pneu
S. pneumoniae prot
Plant SDF encoded
Plant SDF encoded
Plant SDF encoded
Plant SDF encoded
                                                                                                                                                                                                                              Description
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Human herpes virus
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42	A 4 3 C	42	42	42.5	42.5	43	43	43	43	43	43	43	43		43.5	43.5	44	44	44	44	44	44	44	44	44	44	45	45	45	45	45	45.5
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459	269	259	69	965	372	535	535	501	435	378	326	308	286	1874	1098	160	2595	648	648	374	372	372	255	237	139	122	1400	822	354	328	296	125
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AAG24717	AAY08563	AAY35625	AAB44200	AAB42561	AAY72816	AAB65657	AAW77299	AAB54157	AAB00199	AAB65658	AAB60228	AAB36408	AAY35318	AAB76532	AAB76533	AAB29660	AAY39297	AAW96199	AAW96198	AAB58375	AAW04871	AAW04869	AAB58178	AAW73136	AAB61120	AAG03753	AAW82791	AAW73486	AAG24610	AAG24611	AAG24612	AAW28030
Arabidopsis thalia		lamydia pn		Human ORFX ORF2325	ρ.	prot	acid seque	Human pancreatic c	Putative polyunsat	Novel protein kina	Pseudomonas mendoc		Chlamydia pneumoni	Corynebacterium gl	Ф	=			Human herpesvirus-	Lung cancer associ		Cyclin-dependent k	cancer assoc	=	herpesvir	Human secreted pro	Human RON receptor	σ			O)	Staphylococcus aur

ALIGNMENTS

RESULT AAB48241

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Key Location/Qualifiers
Misc-difference 1..552
/note= "Xaa are residues encoded by internal stop codons"
                                                                                                                                                                                                                     Transcription factor; seed storage protein; lectin; oil-body protein; Pv-Seed factor-1; ROM1; Vicilin-box binding protein-1; ROM2; 7S-globulin; phaseolin; PHA-L; bean; nuclear protein; promoter; ORF; bZIP; basic leucine zipper.
WPI; 2001-079619/09
                     Chern M,
                                                               07-OCT-1994;
                                                                                                                                  US6160202-A.
                                                                                                                                                                                                                                                                              Amino acid sequence of bZIP2 ORF1 protein.
                                         (UYMA-) UNIV MARYLAND BALTIMORE COUNTY.
                                                                                      06-FEB-1997;
                                                                                                            12-DEC-2000.
                                                                                                                                                                                                 Phaseolus vulgaris.
                                                                                                                                                                                                                                                                                                   02-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                          AAB48241;
                                                                                                                                                                                                                                                                                                                                               AAB48241 standard; Protein; 552
                     Bustos MM;
                                                                94US-0319544.
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Best Local
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                                                                                                                                                                  Bodmer J,
Irmler M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated transcription factor gene which is expressed in a recombinant maturing dicot seed and which encodes a transcription factor protein which targets a promoter of a gene encoding seed storage proteins, lectins or oil-body proteins. The transcription factors isolated are Pv-Seed factor-1 (ROM1) and Vicilin-box binding protein-1 (ROM2). These factors bind to 7S-globulin (b-phaseolin) or lectin (PHA-L) promoters. The transcription factor gene is useful for enhancing or reducing expression of seed storage protein, lectin or oil-protein genes in dicot seed crops. The present sequence represents the amino acid sequence of bZIP2 (basic leucine zipper) ORF1 protein.
This invention describes novel human and mouse anti-apoptotic gene products which contain at least one death effector domain. The proof the invention are used in the treatment of HIV infections and autolumnune diseases. This sequence represents the human Herpes viru
                                                                 Claim 16;
                                                                                       New DNA encoding for anti-apoptotic infections and autoimmune diseases
                                                                                                                              WPI; 1998-532710/46.
                                                                                                                                                                                                                                               01-APR-1997;
                                                                                                                                                                                                                                                                        01-APR-1997;
                                                                                                                                                                                                                                                                                                  08-OCT-1998
                                                                                                                                                                                                                                                                                                                           DE19713393-A1.
                                                                                                                                                                                                                                                                                                                                                   Human herpes
                                                                                                                                                                                                                                                                                                                                                                            HIV infection;
                                                                                                                                                                                                                                                                                                                                                                                       Death effector domain; human; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                Human herpes virus type 8 FLIP ORF 71 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW76633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW76633 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Columns 31-36; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel transcription factor gene which encodes transcription factor protein that targets promoters of genes encoding seed storage proteins are useful for modulating seed storage protein expression in dicot seed
                                                                                                                                                                                                         (APOT-)
                                                                                                                                                                                                                    (TSCH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 lighihtvkefhphlligll 140
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                                                                                                                                                     Burns K, I
Rimoldi D,
Tschopp J,
                                                              Fig
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                                                                                                                                                                                                                                                                                                                                                    virus
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                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                            autoimmune disease
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                                                              45pp;
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                                                                                                                                                      French EL,
D, Schneider
Hofmann K;
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                                                                                                                                                                  P, Schroeter M,
                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                       anti-apoptotic; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
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                                                                                                     used
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RESULT AAB87615 ID AAB8 XX AAB8 XX AAB8 XX BOV1 XX BOV1 XX BOV1 XX BOV1 XX BOV1 XX BOX BOX XX GEN BA (SEE AA (
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ID AAR5
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                                                                                                                                                                                                                                                                                                                                                                                                      mammary gland cells. The invention is useful for stimulath bovine mammary gland cell growth and function, inhibiting to growth of various mammary gland cancer cells, inhibiting angiogenesis and vascularization of tunours, or modulating the growth of blood vessels in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptides and polynucleotides encoding the polypeptides, which are expressed in bovine mammary gland tissue, useful for stimulating mammary gland growth or function, or inducing differentiation of milk producing cells
                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to proteins derived from bovine mammary gland cells. The invention is useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Havukkala IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200114553-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-2000; 2000WO-NZ00166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENESIS RES & DEV CORP LTD.
(NZPA-) NEW ZEALAND PASTORAL AGRIC
                                                                                                                                                                                                                                          Local Similarity nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 FLIP
                                                                                                                                                                                                                                                                                                                                                               236 AA;
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grigor MR,
                                                                                                                                               67
                                                                                                                                                                                           28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 49.5;
Pred. No. 3
                                                                                                                                                                                                                                                                   Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour; angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molenaar AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #6
                                                                                                                                                                                                                                                                   տ
                                                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                       Length 236;
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188;
                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                          Gaps
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AAR54219

standard;

Protein;

570

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AAY11333
ID AAY1
XX
AC AAX1
AC AAX1
DT 20-1
XX
XX
Str
XX
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XX
Str
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SV
PN WO9-
XX
PF 01-
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                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                 acids in L.lactis subsp. lactis are organised in two units containing the leu and ilv (including ilvD) genes, respectively. Both units are necessary for the synthesis of leucine but only the second unit is required for synthesis of ile and Val. The ilvB and ilvN genes and the subunits of alpha-acetolactate synthase that they code for are claimed.
                                                                                               Streptococcus
streptococcal
  01-APR-1997;
                          09-OCT-1997.
                                               WO9737026-A1
                                                                        Streptococcus
                                                                                                                                   S. pneumoniae
                                                                                                                                                                                 AAY11333;
                                                                                                                                                                                                        AAY11333 standard; Protein; 171
                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The genes involved in the pathway for synthesis of branched amino acids in L lactis subsp. lactis are organised in two units
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA coding for alpha-aceto:lactate synthase - for enhancing di:acetyl prodn. in microorganisms, esp. for mfr. of dairy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-128287/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              attenuation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     branched amino acid; ilv operon; leucine; isoleucine; valine; biosynthesis; alpha-acetolactate synthase; diacetyl; food flavouring;
                                                                                                                                                           20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FR2696190-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehrlich S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L.lactis branched amino acid synthesis ilvD gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR54219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INRG ) INRA INST NAT RECH AGRONOMIQUE (AGRI-) AGRIC & FOOD RES COUNCIL.
                                                                                                                                                                                                                                                                 ||||| :| |:||:
495 hivpeaveggliglv 509
                                                                                                                                                                                                                                                                                        9 HIVPEFIESQLLGLL 23
                                                                                                                                                                                                                               ഗ
                                                                                                                                                                                                                                                                                                                 Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ64211.
                                                                                                                                                                                                                                                                                                                                                                           570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F1g 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Godon J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lactis (subsp. lactis).
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-terminator; Lactococcus.
                                                                                                                                                        (first entry)
                                                                                               pneumoniae strain 0100993;
infection; pneumococcal.
                                                                                                                                protein SEQ ID
                                                                        pneumoniae
                                                                                                                                                                                                                                                                                                                                                                           A,
  97WO-US05306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92FR-0011470.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45pp; French.
                                                                                                                                                                                                                                                                                                                            34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Renault P;
                                                                                                                                                                                                                                                                                                               Score 49; DB
Pred. No. 15;
3; Mismatches
                                                                                                                                  NO:443.
                                                                                                                                                                                                         B
                                                                                                          vaccine;
                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                 Ψ
                                                                                                                                                                                                                                                                                                                                        Length 570;
                                                                                                          immune response;
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RESULT
AAW38569
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Best Local s
Matches
                                                                                                                                                                                                                  Streptococcus pneumoniae protein; genetic immunisation; ar immunological response; inoculation; antibody production; T cell immune response; antimicrobial compound; bacterial extracellular matrix protein; protein-mediated cell invasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX30724 to AAX30946 represent genomic DNA sequences isolated from Streptococcus pneumoniae strain 0100993. These genomic DNA sequences encode the novel proteins given in AAY11114 to AAY11367. The proteins, isolated from Streptococcus pneumoniae, can be used in vaccines against streptococcal infections and in assays for identifying compounds that inhibit or activate the activity of the proteins. The antagonists can be used to treat an individual having need to inhibit a bacterial
                                                      (SMIK )
WPI; 1998-008793/01
                     Stodola RK;
                                Black MT,
                                                                                                               14-MAY-1997;
                                                                                                                                                              WO9743303-A1
                                                                                                                                                                                     Streptococcus
                                                                                                                                                                                                          pathogenesis.
                                                                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                      06-NOV-1998
                                                                                                                                                                                                                                                                                                                             AAW38569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 325; 354pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccines, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Black MT,
Stodola RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-AUG-1996;
02-APR-1996;
                                                                                           14-MAY-1996;
                                                                                                                                       20-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                  AAW38569 standard; Protein; 173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein. Vectors expressing the proteins can be used to induce a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding pneumococcal polypeptide(s) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-503111/46.
N-PSDB; AAX30915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM CORP (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                              90
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                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                          CVLGYLHIVPEFIESQLLGLLSPVSL 28
                                                       SMITHKLINE BEECHAM CORP. SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 34.6
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hodgson JE,
                                Hodgson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1mmune
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                    pneumoniae
                                                                                                                                                                                                                                                                             pneumoniae protein of unknown function.
                                                                                           96US-0017670
                                                                                                                97WO-US07950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0025788.
96US-0014690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       response in mammals.
                                 JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.78;
                                   Knowles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47.5; DB Pred. No. 6.3; 9; Mismatches
                                 DJC,
                                   Nicholas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicholas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                   RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                       invasion; wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful
                                                                                                                                                                                                                                                      antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171;
                                                                                                                                                                                                                                 ; inhibitor; l adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۲,
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N-PSDB; AAT98621

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AAW80687
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AC AAW8
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AC CAMA
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AC CAMA
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KW Viru
KW Wiri
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Pi Skatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a Streptococcus pneumoniae protein of cunknown function, and is encoded by a DNA sequence of the invention. The DNA sequences were isolated from Streptococcus pneumoniae strain collops (NCIMB 40794). The Streptococcus pneumoniae proteins of the invention can be used to identify compounds which interact with and contract the activity of the proteins. Antagonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic immunisation. They can also be used to induce an immunological response in a mammal by inoculation with the S. pneumoniae proteins or delivery of the encoding nucleic acids in a vector adequate to produce antibody and/or T cell immune responses to protect the animal from disease. The proteins can also be used to identify antimicrobial compounds which are capable of inhibiting their bloactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian extracellular matrix proteins on in-dwelling devices or in wounds, to block protein-mediated mammalian cell invasion, and to block the normal progression of pathogenesis in infections initiated other than by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
                                                                                                                                         Mills BJ,
Skatrud PI
                                                                                                                                                                      Baltz
Mills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW80687;
                                                                                                                                                                                                                                                                                                             13-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip; virulence; antibody; infection; detection; treatment; hypothetical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S. pneumoniae protein of unknown function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW80687 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 342; 483pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel Streptococcus pneumoniae proteins and related DNA - useful diagnosing anti-microbial agents for treatment of bacterial
                               N-PSDB;
                                                         WPI; 1998-348529/30
                                                                                                                                                                                                                                                                                                                                                                    09-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virulence; antibody; infection; detection; treatment; hypothetical
cell wall biosynthetic, external target; minimal gene set protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                          Young Bellido ML;
                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9826072-A1
                                                                                                                                                                                                                                                    (ELIL ) LILLY & CO ELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 clyghlhvpsawlegkil-flnpgsi 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CVLGYLHIVPEFIESQLLGLLSPVSL 28
                               AAV65255
                                                                                                                                         PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9;
                                                                                                                                       Burgett SG,
Norris FH,
Smith MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae.
                                                                                                                                                                                                                                                                                                          96US-0036281
                                                                                                                                                                                                                                                                                                                                                                    97WO-US22578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.7%;
34.6%;
                                                                                                                                       Peery RB,
Solenberg
                                                                                                                                                                                             Dehoff BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47.5;
Pred. No. 6.
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                                                                                                                                       Rockey PK, Ro
PJ, Treadway
                                                                                                                                                                                             Hoskins JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                       Rosteck PR;
ay PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                             Jaskunas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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106

clyghlhvpsawmegkil-finpgsi 130

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δÃ
                                                           Query Match
Best Local
                                         Matches
                                                                                                                                                                                            set proteins. A recombinant host containing a vector comprising any of the above nucleic acids can be used for the recombinant expression of the proteins. The invention also provides a DNA chip having arrayed on it at least 15 base pair fragment of any one or more of these DNA sequences. The DNA chip can be used methods for evaluating gene expression in S. pneumoniae and for identifying virulence genes in S. pneumoniae. Antibodies that selectively bind to the above proteins or peptide fragments can be used to treat S. pneumoniae, infection. The antibodies
                                                                                                                                                                                                                                                                                                                                                         from the Streptococcus pneumoniae genome and corresponding protein sequences (AAW80605 to AAW80728). The protein sequences are classified hypothetical, cell wall biosynthetic, external target, or minimal gene
                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae nucleic acid sequences - used in DNA chips for evaluating gene expression, and identification of virulence
                                                                                                                                                                                 can also be used to detect S. pneumoniae cells.
                                                                                                                                                                                                                                                                                                                                                                                                                     function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes
3 CVLGYLHIVPEFIESQLLGLLSPVSL 28
                                                                                                                                                                                                                                                                                                                                                                                                                       sequence represents a Streptococcus pneumoniae protein of unknown tion. The invention provides DNA sequences (AAV65201 to AAV65304)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Pages 275-276; 333pp; English.
                                         Similarity
9; Conser
                                                                                                                                            173 AA;
                                         Conservative
                                                           33.0%;
                                         9;
                                                           Score 46.5;
Pred. No. 9
                                         Mismatches
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ω
                                                                                  멂
                                                                                19;
                                         7;
                                                                              Length 173;
                                             Indels
                                           1;
                                         Gaps
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AAB24844
Claim 14; Page 486; 673pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant; corn; Arabidopsis thaliana; sequence-determined DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant SDF encoded polypeptide sequence SEQ List 1 NO:339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB24844;
                                   expression of a target gene
                                                                                                                                            Alexandrov N,
Zheng L;
                                                                                                                                                                                                                                                                      07-JAN-2000; 2000WO-US00466
                                                                                                                                                                                                                                                                                                         13-JUL-2000
                                                                                                                                                                                                                                                                                                                                          WO200040695-A2
                                                                                                                                                                                                                                                                                                                                                                               Plant.
                                                                                                                                                                                                                                                                                                                                                                                                                untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB24844 standard; Peptide; 127
                                                     fragments,
                                                                    New corn plant and Arabidopsis thaliana sequence-determined DNA
                                                                                                         WPI; 2000-465970/40
                                                                                                                                                                                                (CERE-) CERES INC.
                                                                                                                                                                                                                                     08-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                 genetic
                                                     useful for expressing
                                                                                                                                                                                                                                                                                                                                                                                                               mapping; identification; promoter; structural
region; expression control.
                                                                                                                                                              Brover V,
                                                                                                                                                                                                                                     99US-0115293
                                                                                                                                                             Chen
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                                                     gene
                                                                                                                                                              Subramanian G,
                                                     products
                                                       and
                                                       for controlling
                                                                                                                                                                Troukhan ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                 fragment;
gene; UTR;
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The present invention describes polynucleotides, such as complete cDNA sequences and/or sequences of genomic DNA encompassing complete genes, portions of genes, and/or intergenic regions, collectively referred to

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AAB24843
ID AAB2
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Matches 7
sequences and/or sequences of genomic DNA encompassing complete genes portions of genes, and/or intergenic regions, collectively referred t as sequence-determined DNA fragments (Egions, collectively referred t as sequence-determined DNA fragments (From corn plants and Arabidopsis thaliana. The SDFs are promoters, structural genes, untranslated regions (UTRs), or 3' termination sequences. They can be used for expressing a gene product and controlling expression of a target gene, either as a promoter, a structural gene, an UTR or as a 3' termination sequence. They are also useful as tools for genetic mapping, and identification of a particular individual plant or for clustering a group pf plants with a common trait. AAA78433 to AAA7863 and AAB24605 to AAB25099 represent the specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant;
SDF; g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as sequence-determined DNA fragments (SDFs), from corn plants and Arabidopsis thaliana. The SDFs are promoters, structural genes, untranslated regions (UTRs), or 3' termination sequences. They can be used for expressing a gene product and controlling expression of a target gene, either as a promoter, a structural gene, an UTR or as a 3' termination sequence. They are also useful as tools for genetic mapping, and identification of a particular individual plant or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mapping, and identification of a particular individual plant or for clustering a group pf plants with a common trait. AAA78433 to AAA78630 and AAB24605 to AAB25099 represent the specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDF; genetic mapping;
untranslated region;
                                                                                                                                                                                                                                                                                      The present invention describes polynucleotides, such as complete cDNA
                                                                                                                                                                                                                                                                                                                                   Claim 14; Page 485-486; 673pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alexandrov N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant SDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB24843 standard; Peptide; 169 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       New corn plant and Arabidopsis thaliana sequence-determined DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CERE-) CERES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 36.1 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    φ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       t; corn; Arabidopsis thaliana; sequence-determined DNA
genetic mapping; identification; promoter; structural
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                                                                                                                                                                                                                                                                                                                                                                                       useful for expressing gene products and of a target gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.6%;
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                                                                                                                                                                                                                                                                                                                                                                                     gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptides encoded by them given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  control.
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7.9;
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                                                                                                                                                                                                                                                                                                                                                                                                               for controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Troukhan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragment;
gene; UTR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene;
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                                                                                                                                                                                                                                                            genes,
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Query Match Best Local S Matches 7

Similarity 36.
7; Conservative

32.6%;

Score 46; DB Pred. No. 12; 7; Mismatches

21;

Length 181;

5;

Indels

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Gaps

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RESULT 1
AAB24842
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Best Local
                                             sequences and/or sequences of genomic DNA encompassing complete genes, portions of genes, and/or intergenic regions, collectively referred to as sequence-determined DNA fragments (SDFs), from corn plants and Arabidopsis thaliana. The SDFs are promoters, structural genes, untranslated regions (UTRs), or 3' termination sequences. They can be used for expressing a gene product and controlling expression of a target gene, either as a promoter, a structural gene, an UTR or as a 3' termination sequence. They are also useful as tools for genetic mapping, and identification of a particular individual plant or for clustering a group pf plants with a common trait. AAA78433 to AAA78630 and AAB24605 to AAB25099 represent the specifically claimed
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SDF; ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide sequences and present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB24842 standard; Peptide; 181 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
                                   polynucleotide sequences
                                                                                                                                                                                           The present invention describes polynucleotides, such as complete cDNA
                                                                                                                                                                                                                  Claim 14; Page 485; 673pp; English
                                                                                                                                                                                                                                                                      New corn plant and Arabidopsis thaliana sequence-determined DNA
                                                                                                                                                                                                                                                                                                 WPI; 2000-465970/40
                                                                                                                                                                                                                                                                                                                         Zheng
                                                                                                                                                                                                                                                                                                                                     Alexandrov N,
                                                                                                                                                                                                                                                                                                                                                                                       08-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 HIVPEFIESQLLGLLSPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            corn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 7; Conserv
                         invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoded polypeptide
                                                                                                                                                                                                                                           useful for expres
of a target gene
181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana; sequence-determined DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                      Brover
                                                                                                                                                                                                                                                                                                                                                                                         9905-0115293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression control
                                                                                                                                                                                                                                                                                                                                      <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identification;
                                     represent the specifically claimed and polypeptides encoded by them g
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                                                                                                                                                                                                                                                                                                                                      Chen
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Pred.
                                   polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence SEQ List 1 NO:337.
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                                                                                                                                                                                                                                                         gene
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                                                                                                                                                                                                                                                                                                                                      Subramanian
                                                                                                                                                                                                                                                          products and for controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter; structural gene; UTR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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                                                                                                                                                                                                                                                                                                                                      Troukhan ME;
                                      given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                  RESULT 11
AAB90659
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                                                                                                                                          The present sequence is provided in a specification relating to nucleic CC acid molecules encoding 32 novel human secreted polypeptides. The nucleic CC acid molecules and polypeptides may be used in the prevention, diagnosis CC and treatment of diseases such as immune disorders (e.g. multiple CC sclerosis, systemic lupus erythematosus and human immuno-deficiency virus CC (HIV) infections), hyperproliferative disorders (e.g. cancers and CC Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome, CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic CC disorders (e.g. corneal graft neovascularisation and diabetic CC retinopathy), neurological disorders (e.g. Huntington's chorea, CC Alphalmer's disease and Parkinson's disease) infectious diseases and/or CC acid molecules may be used to produce the secreted polypeptides. They may also be used as DNA probes in diagnostic assays to detect and quantitate CC corporation of similar nucleic acid sequences in samples. The CC polypeptides may be used as antigens in the production of antibodies and cc in assays to identify modulators of their expression and activity.
                                  Matches
                                                                Query Match
                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding 32 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antimicrobial; vulnerary; vaccine; gene therapy; cancer;
protein coordinate data; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toad; lipocalin; secreted protein; immunomodulatory; antisclerotic; dermatological; antiinflammatory; anti-HIV; cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotectant; nootropic; anticonvulsant; antialzheimers; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bufo marinus lipocalin protein, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2; 890pp; English.
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                                Conservative
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re PA, Olsen HS,
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47.4%;
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Pred. No.
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Rosen CA, Ruben
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                               Gaps
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AAG24612 ID AAG2

AAG24612 standard; Protein; 296 AA

AAG24612;

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RESULT 12
AAW28030
ID AAW28(
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                   The present sequence represents a Staphylococcus aureus protein of unknown function. The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Black MT,
Pratt JM,
                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 419; 989pp; English
                                                                                                                                                                                                                                                                                                                                                                     Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 to isolate antimicrobial compounds, and in vaccines against Saureus infection {\bf v}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus protein; ribozyme; antisense Staphylococcal gene; regulatory element; bacterial vaccine; Staphylococcal infection; food poisoning;
                                                                                                                             Sequence
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                                                                      Score 45.5;
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gene expression;
scaled skin syndrome;
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RESULT 1
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36 Ylhifpqflen 246
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                  EP1033405-A2
                                   Arabidopsis thaliana
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68 ylhifpqflen 278
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                                                              on; signal transduction pathway; metabolic pathway;
genetic mapping; gene expression control; promoter;
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